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(54) EXPRESSION OF RECOMBINANT FUSION PROTEINS IN ATTENUATED BACTERIA

EXPRESSION REKOMBINANTER FUSIONSPROTEINE IN ATTENUIERTEN BAKTERIEN

EXPRESSION DE PROTEINES RECOMBINANTES FUSIONNEES DANS DES BACTERIES
ATTENUEES

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peptides'**

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Description

This invention relates to vaccine compositions containing attenuated bacteria.

In recent years, there has emerged a new generation of live oral salmonella vaccines based upon strains of Salmonella which have been attenuated by the introduction of a non-reverting mutation in a gene in the aromatic biosynthetic pathway of the bacterium. Such strains are disclosed, for example, in EP-A-0322237. The aforesaid live oral salmonella vaccines are showing promise as vaccines for salmonellosis in man and animals, and they can also be used effectively as carriers for the delivery of heterologous antigens to the immune system. Combined salmonella vaccines have been used to deliver antigens from viruses, bacteria, and parasites, eliciting secretory, humoral and cell-mediated immune responses to the recombinant antigens. Combined salmonella vaccines show great potential as single dose oral multivaccine delivery systems [C, Hormaeche *et al*, FEMS Symposium No. 63, Plenum, New York; pp 71-83, 1992].

There are problems to be overcome in the development of combined salmonella vaccines. A major consideration is obtaining a high level of expression of the recombinant antigen in the salmonella vaccine so that it will be sufficient to trigger an immune response. However, unregulated high level expression of foreign antigens can be toxic and affect cell viability [I. Charles and G. Dougan, TIBTECH 8, pp 117-21, 1990], rendering the vaccine ineffective or causing loss of the recombinant DNA. Several possible solutions to this problem have been described, such as expression from plasmids carrying essential genes, "on-off" promoters or incorporation of the foreign genes into the salmonella chromosome.

An alternative approach to overcoming the aforesaid problem would be to use a promoter which is inducible *in vivo*, and one such promoter is the E.coli nitrite reductase promoter nirB which is induced under anaerobiosis and has been used in biotechnology for the production of tetanus toxin fragment C (TetC) of Clostridium tetani [M.D. Oxer *et al* Nucl. Ac. Res., 19, pp 2889-92, 1991]. It has previously been found by the inventors of this application (S.N. Chatfield *et al* Bio/Technology, Vol. 10, pp 888-92 1992) that an Aro Salmonella harbouring a construct expressing TetC from the nirB promoter (pTETnir15) elicited very high anti-tetanus antibody responses in mice. The article by Chatfield *et al* was published after the priority date of this application.

However, we have also found that when it was attempted to express the P28 antigen from Schistosoma mansoni alone from nirB, the resulting construct was not immunogenic.

Tetanus toxoid has been extensively used as an adjuvant for chemically coupled guest epitopes [D.A. Herrington *et al*. Nature, 328, pp 257-9 1987]. The potent immunogenicity of TetC in Salmonella suggested to us that it may be possible to exploit this character to promote the immune response of the guest peptides or proteins. However, fusing two proteins together often leads to an incorrectly folded chimaeric protein which no longer retains the properties of the individual components. For example the B subunit of the Vibrio cholerae (CT-B) and E.coli (LT-B) enterotoxins are powerful mucosal immunogens but genetic fusions to these subunits can alter the structure and properties of the carrier and hence their immunogenicity [see M. Sandkvist *et al*. J. Bacteriol 169, pp 4570-6, 1987, Clements 1990 and M. Lipscombe *et al* [Mol. Microbiol 5, pp 1385 1990]. Moreover, many heterologous genes expressed in bacteria are not produced in soluble properly folded, or active forms and tend to accumulate as insoluble aggregates [see C. Schein *et al*. Bio/Technology 6, pp 291-4, 1988 and R. Halenbeck *et al*; Bio/Technology 7, pp 710-5, 1989].

It is an object of the invention to overcome the aforementioned problems.

We have now found that efficient expression of recombinant antigens, and in particular fusion proteins, can be achieved in bacteria such as salmonellae, by the use of an inducible promoter such as nirB and by incorporating a flexible hinge region between two antigenic components of the fusion protein. The resulting recombinant antigens have been shown to have good immunogenicity. It has also been found, surprisingly, that enhanced expression of a protein can be obtained when a gene coding for the protein is linked to the gene for tetanus toxin C fragment.

Accordingly, in a first aspect, the present invention provides a vaccine composition comprising a pharmaceutically acceptable carrier and an attenuated bacterium containing a DNA construct comprising a promoter which is capable of promoting expression of a sequence under, and has activity which is induced under, anaerobic conditions, the promoter being operably linked to a DNA sequence encoding first and second proteins linked by a chain of amino acids defining a hinge region.

A preferred promoter is the nirB promoter or a part or derivative thereof which is capable of promoting expression of a sequence under anaerobic conditions.

Other particular and preferred aspects of the invention are as defined in the dependent claims appended hereto.

The first and second proteins are preferably heterologous proteins and in particular can be polypeptide immunogens; for example they may be antigenic sequences derived from a virus, bacterium, fungus, yeast or parasite. In particular, it is preferred that the first said protein is an antigenic sequence comprising tetanus toxin fragment C or epitopes thereof.

The second protein is preferably an antigenic determinant of a pathogenic organism. For example, the antigenic determinant may be an antigenic sequence derived from a virus, bacterium, fungus, yeast or parasite.

Examples of viral antigenic sequences for the first and/or second heterologous proteins are sequences derived from a type of human immuno-deficiency virus (HIV) such as HIV-1 or HIV-2, the CD4 receptor binding site from HIV, for example from HIV-1 or -2, hepatitis A or B virus, human rhinovirus such as type 2 or type 14, Herpes simplex virus, poliovirus type 2 or 3, foot-and-mouth disease virus (FMDV), rabies virus, rotavirus, influenza virus, coxsackie virus, human papilloma virus (HPV), for example the type 16 papilloma virus, the E7 protein thereof, and fragments containing the E7 protein or its epitopes; and simian immunodeficiency virus (SIV). Examples of antigens derived from bacteria are those derived from Bordetella pertussis (e.g. P69 protein and filamentous haemagglutinin (FHA) antigens), Vibrio cholerae, Bacillus anthracis, and E.coli antigens such as E.coli heat Labile toxin B subunit (LT-B), E.coli K88 antigens, and enterotoxigenic E.coli antigens. Other examples of antigens include the cell surface antigen CD4, Schistosoma mansoni P28 glutathione S-transferase antigens (P28 antigens) and antigens of flukes, mycoplasma, roundworms, tapeworms, Chlamydia trachomatis, and malaria parasites, e.g. parasites of the genus plasmodium or babesia, for example Plasmodium falciparum, and peptides encoding immunogenic epitopes from the aforementioned antigens.

Particular antigens include the full length Schistosoma mansoni P28, and oligomers (e.g. 2, 4 and 8-mers) of the immunogenic P28 aa 115-131 peptide (which contains both a B and T cell epitope), and human papilloma virus E7 protein, Herpes simplex antigens, foot and mouth disease virus antigens and simian immunodeficiency virus antigens.

The promoter sequence has activity which is induced in response to a change in the surrounding environment, i.e. is induced by anaerobic conditions. A particular example of such a promoter sequence is the nirB promoter which has been described, for example in International Patent Application WO-A-92/15689. The nirB promoter has been isolated from E.coli, where it directs expression of an operon which includes the nitrite reductase gene nirB (Jayaraman *et al*, J. Mol. Biol. 196, 781-788, 1987), and nirD, nirC, cysG (Peakman *et al*, Eur. J. Biochem. 191, 315-323, 1990). It is regulated both by nitrite and by changes in the oxygen tension of the environment, becoming active when deprived of oxygen, (Cole, Biochem, Biophys. Acta. 162, 356-368, 1968). Response to anaerobiosis is mediated through the protein FNR, acting as a transcriptional activator, in a mechanism common to many anaerobic respiratory genes. By deletion and mutational analysis the part of the promoter which responds solely to anaerobiosis has been isolated and by comparison with other anaerobically-regulated promoters a consensus FNR-binding site has been identified (Bell *et al*, Nucl. Acids. Res. 17, 3865-3874, 1989; Jayaraman *et al*, Nucl. Acids. Res. 17, 135-145, 1989). It has also been shown that the distance between the putative FNR-binding site and the -10 homology region is critical (Bell *et al*, Molec. Microbiol. 4, 1753-1763, 1990). It is therefore preferred to use only that part of the nirB promoter which responds solely to anaerobiosis. As used herein, references to the nirB promoter refer to the promoter itself or a part or derivative thereof which is capable of promoting expression of a coding sequence under anaerobic conditions. The preferred sequence, and which contains the nirB promoter is: AATTCAAGTAAATTGATGTACATCAAAT-GGTACCCCTTGCTGAATCGTTAAGG TAGGCCGGTAGGGCC (SEQ ID NO: 1)

The hinge region is a region designed to promote the independent folding of both the first and second proteins by providing both spatial and temporal separation between the domains.

The hinge region typically is a sequence encoding a high proportion of proline and/or glycine amino acids. The hinge region may be composed entirely of proline and/or glycine amino acids. The hinge region may comprise one or more glycine-proline dipeptide units.

The hinge region may, for example, contain up to about fifteen amino acids, for example at least 4 and preferably 6-14 amino acids, the number of amino acids being such as to impart flexibility between the first and second proteins.

In one embodiment, the hinge region can correspond substantially to the hinge domain of an antibody immunoglobulin. The hinge regions of IgG antibodies in particular are rich in prolines [T.E. Michaelson *et al*. J. Biol. Chem. 252, 883-9 1977], which are thought to provide a flexible joint between the antigen binding and tail domains.

Without wishing to be bound by any theory, the prolines are thought to form the rigid part of the hinge as the ring structure characteristic of this amino acid hinders rotation around the peptide bond that connects the proline residue with an adjacent amino acid. This property is thought to prevent proline, and adjacent residues, from adopting the ordered structure of an alpha helix or beta strand. Flexibility is thought to be imparted by glycine, the simplest amino acid, with very limited steric demands. Glycine is thought to function as a flexible elbow in the hinge. Other amino acids may be substituted for glycine, particularly those without bulky side-chains, such as alanine, serine, asparagine and threonine.

In one preferred embodiment, the hinge region is a chain of four or more amino acids defining the sequence



wherein Pro is proline, X and Y are each glycine, or an amino acid having a non-bulky side chain; Z is any amino acid; p is a positive integer; q is a positive integer of from one to ten; and r is zero or a positive integer greater than zero.

The hinge region can be a discrete region heterologous to both the first and second proteins or can be defined by a carboxy-end portion of the first protein or an amino-end portion of the second protein.

5 Codons which are infrequently utilised in E.coli [H. Grosjean *et al*, Gene 18, 199-209, 1982] and Salmonella are selected to encode for the hinge, as such rare codons are thought to cause ribosomal pausing during translation of the messenger RNA and allow for the correct folding of polypeptide domains [I.J. Purvis *et al*. J. Mol. Biol. 193, 413-7 1987]. In addition, where possible restriction enzymes are chosen for the cloning region which, when translated in the resulting fusion, do not encode for bulky or charged side-groups.

In a preferred embodiment of the invention, the nirB promoter sequence is operably linked to a DNA sequence encoding first and second polypeptide immunogens linked by a hinge region, wherein the first polypeptide immunogen comprises tetanus toxin fragment C or epitopes thereof.

10 It has been found that by providing a DNA sequence encoding tetanus toxin fragment C (TetC) linked via a hinge region to a second sequence encoding an antigen, the expression of the sequence in bacterial cells is enhanced relative to constructs wherein the fragment C and hinge region are absent. For example, the expression level of the full length P28 protein of S. mansoni when expressed as a fusion to TetC was greater than when the P28 protein was expressed alone from the nirB promoter. The TetC fusions to the full lenght P28 protein of S. mansoni and its tandem epitopes were all soluble and expressed in both E.coli and S.typhimurium. In addition, the TetC-P28 fusion protein was capable of being affinity purified by a glutathione agarose matrix, suggesting that the P28 had folded correctly to adopt a conformation still capable of binding to its natural substrate.

15 Stable expression of the first and second heterologous proteins linked by the hinge region can be obtained *in vivo*. The heterologous proteins can be expressed in an attenuated bacterium which can thus be used as a vaccine.

20 The attenuated bacterium may be selected from the genera Salmonella, Bordetella, Vibrio, Haemophilus, Neisseria and Yersinia. Alternatively, the attenuated bacterium may be an attenuated strain of enterotoxigenic Escherichia coli. In particular the following species can be mentioned: S.typhi - the cause of human typhoid; S.typhimurium - the cause of salmonellosis in several animal species; S.enteritidis - a cause of food poisoning in humans; S.choleraesuis - a cause of salmonellosis in pigs; Bordetella pertussis - the cause of whooping cough; Haemophilus influenzae - a cause of meningitis; Neisseria gonorrhoeae - the cause of gonorrhoea; and Yersinia - a cause of food poisoning.

25 Attenuation of the bacterium may be attributable to a non-reverting mutation in a gene in the aromatic amino acid biosynthetic pathway of the bacterium. There are at least ten genes involved in the synthesis of chorismate, the branch point compound in the aromatic amino acid biosynthetic pathway. Several of these map at widely differing locations on the bacterial genome, for example aroA (5-enolpyruvylshikimate-3-phosphate synthase), aroC (chorismate synthase), aroD (3-dihydroquinate dehydratase) and aroE (shikimate dehydrogenase). A mutation may therefore occur in the aroA, aroC, aroD, or aroE gene.

30 Preferably, however, an attenuated bacterium harbours a non-reverting mutation in each of two discrete genes in its aromatic amino acid biosynthetic pathway. Such bacteria are disclosed in EP-A-0322237. Double aro mutants which are suitable are aroA aroC, aroA aroD, and aroA aroE. Other bacteria having mutations in other combinations of the aroA, aroC, aroD and aroE genes are however useful. Particularly preferred are Salmonella double aro mutants, for example double aro mutants of S.typhi or S.typhimurium, in particular aroA aroC, aroA aroD and aroA aroE mutants. Alternatively, the attenuated bacterium may harbour a non-reverting mutation in a gene concerned with the regulation of one or more other genes (EP-A-0400958). Preferably the mutation occurs in the ompR gene or another gene involved in regulation. There are a large number of other genes which are concerned with regulation and are known to respond to environmental stimuli (Ronson *et al*, Cell 49, 579-581).

35 This type of attenuated bacterium may harbour a second mutation in a second gene. Preferably the second gene is a gene encoding for an enzyme involved in an essential biosynthetic pathway, in particular genes involved in the pre-chorismate pathway involved in the biosynthesis of aromatic compounds. The second mutation is therefore preferably in the aroA, aroC or aroD gene.

40 Another type of attenuated bacterium is one in which attenuation is brought about by the presence of a non-reverting mutation in DNA of the bacterium which encodes, or which regulates the expression of DNA encoding, a protein that is produced in response to environmental stress. Such bacteria are disclosed in WO 91/15572. The non-reverting mutation may be a deletion, insertion, inversion or substitution. A deletion mutation may be generated using a transposon.

45 The vaccine composition of the invention may comprise one or more suitable adjuvants. The vaccine composition is advantageously presented in a lyophilised form, for example in a capsular form, for oral administration to a patient. Such capsules may be provided with an enteric coating comprising, for example, Eudragit "S", Eudragit "L", Cellulose acetate, Cellulose acetate phthalate or hydroxypropylmethyl Cellulose. These capsules may be used as such, or alternatively, the lyophilised material may be reconstituted prior to administration, e.g. as a suspension. Reconstitution is advantageously effected in buffer at a suitable pH to ensure the viability of the organisms. In order to protect the attenuated bacteria and the vaccine from gastric acidity, a sodium bicarbonate preparation is advantageously administered before each administration of the vaccine. Alternatively, the vaccine may be prepared for parenteral administration, intranasal administration or intramammary administration.

50 The vaccine composition of the invention may be used in the prophylactic treatment of a host, particularly a human

host but also possibly an animal host. An infection caused by a micro-organism, especially a pathogen, may therefore be prevented by administering an effective dose of an attenuated bacterium in a vaccine composition according to the invention. The bacterium then expresses a heterologous protein or proteins capable of raising antibody to the micro-organism. The dosage employed will be dependent on various factors including the size and weight of the host, the type of vaccine formulated and the nature of the heterologous protein.

An attenuated bacterium useful in a vaccine composition according to the present invention may be prepared by transforming an attenuated bacterium with a DNA construct as hereinbefore defined. Any suitable transformation technique may be employed, such as electroporation. In this way, an attenuated bacterium capable of expressing a protein or proteins heterologous to the bacterium may be obtained. A culture of the attenuated bacterium may be grown under aerobic conditions. A sufficient amount of the bacterium is thus prepared for formulation as a vaccine, with minimal expression of the heterologous protein occurring.

The DNA construct may be a replicable expression vector comprising the nirB promoter operably linked to a DNA sequence encoding the tetanus toxin C fragment or epitopes thereof and the second heterologous protein, linked by a hinge region. The nirB promoter may be inserted in an expression vector, which already incorporates a gene encoding one of the heterologous proteins (e.g. tetanus toxin C fragment), in place of the existing promoter controlling expression of the protein. The hinge region and gene encoding the second heterologous protein (e.g. an antigenic sequence) may then be inserted. The expression vector should, of course, be compatible with the attenuated bacterium into which the vector is to be inserted.

The expression vector is provided with appropriate transcriptional and translational control elements including, besides the nirB promoter, a transcriptional termination site and translational start and stop codons. An appropriate ribosome binding site is provided. The vector typically comprises an origin of replication and, if desired, a selectable marker gene such as an antibiotic resistance gene. The vector may be a plasmid.

The invention will now be illustrated but not limited, by reference to the following examples and the accompanying drawings, in which:

Figure 1 is a schematic illustration of the construction of an intermediate plasmid pTECH1 in accordance with one aspect of the invention.
 Figure 2 is a schematic illustration of the construction of a second intermediate plasmid pTECH2.
 Figure 3 is a schematic illustration of the construction of a plasmid of the invention using the intermediate plasmid of Figure 2 as the starting material. In Figure 3 B = BamH I, E = EcoR V; H = Hind III; X = XbaI; S = SphI.
 Figure 4 is a schematic illustration of the construction of a plasmid containing repeating epitopes (repitopes).
 Figure 5 illustrates antibody responses against recombinant S. mansoni protein P28 as detected by ELISA in mice inoculated intravenously with SL3261, SL3261(pTETnir15), SL3261 (pTECH2), SL3261(pTECH2-monomer), SL3261 (pTECH2-dimer), SL3261(pTECH2-tetramer), SL3261(pTECH2-octamer), and SL3261(pTECH1-P28). In Figure 5 the results are expressed as OD in individual mice at intervals after immunisation.
 Figure 6 illustrates antibody responses against TetC as detected by ELISA in mice inoculated as in Figure 5.
 Figure 7 illustrates antibody responses against peptide 115-131 of the P28 protein coupled to ovalbumin as detected by ELISA in mice inoculated intravenously with SL3261, SL3261(pTECH2), SL3261(pTECH2-monomer), SL3261(pTECH2-dimer), SL3261(pTECH2-tetramer), and

SL3261(pTECH2-octamer).

Figure 8 illustrates antibody responses against TetC as detected by ELISA from mice inoculated orally with SL3261 (pTECH1-P28).
 Figure 9 illustrates antibody responses against recombinant P28 as detected by ELISA in mice inoculated as in Figure 8.

Figure 10 illustrates schematically the preparation of various constructs from the pTECH2 intermediate plasmid.
 Figure 11 illustrates schematically the structure of tripartite protein structures ("heteromers") prepared using pTECH2.
 Figure 12 shows the DNA sequence of the vector pTECH1. (SEQ ID NO: 17).
 Figure 13 shows the DNA sequence of the vector pTECH2. (SEQ ID NO: 18).
 Figure 14 illustrates, schematically, the restriction sites on the vector pTECH2.

EXAMPLE 1

Preparation of pTECH1

The preparation of pTECH1, a plasmid incorporating the nirB promoter and TetC gene, and a DNA sequence

encoding a hinge region and containing restriction endonuclease sites to allow insertion of a gene coding for a second or guest protein, is illustrated in Figure 1. Expression plasmid pTETnir15, the starting material shown in Figure 1, was constructed from pTETtacI5 (Makoff *et al*, Nucl. Acids Res. 17 10191-10202, 1989); by replacing the EcoRI-Apal region (1354bp) containing the lacI gene and tac promoter with the following pair of oligos 1 and 2:

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Oligo-1 5' AATTCAAGGTAAATTTGATGTACATCAAATGGTACCCCTTGCTGAAT

10

Oligo-2 3' -GTCCATTAAACTACATGTAGTTACCATGGGAACGACTTA

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CGTTAAGGTAGGCAGGTAGGGCC-3' (SEQ ID NO: 2)

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The oligonucleotides were synthesised on a Pharmacia Gene Assembler and the resulting plasmids confirmed by sequencing (Makoff *et al*, Bio/Technology 7, 1043-1046, 1989).

25

The pTETnir15 plasmid was then used for construction of the novel pTECH1 plasmid incorporating a polylinker region suitable as a site for insertion of heterologous DNA to direct the expression of fragment C fusion proteins. pTETnir15 is a known pAT153-based plasmid which directs the expression of fragment C. However, there are no naturally occurring convenient restriction sites present at the 3'-end of the TetC gene. Therefore, target sites, preceded by a hinge region, were introduced at the 3'-end of the TetC coding region by means of primers tailored with "add-on" adapter sequences (Table 1), using the polymerase chain reaction (PCR) [K. Mullis *et al*, Cold Spring Harbor Sym. Quant. Biol. 51, 263-273 1986]. Accordingly, pTETnir15 was used as a template in a PCR reaction using primers corresponding to regions covering the SacII and BamHI sites. The anti-sense primer in this amplification was tailored with a 38 base 5'-adaptor sequence. The anti-sense primer was designed so that a sequence encoding novel XbaI, SpeI and BamHI sites were incorporated into the PCR product. In addition, DNA sequences encoding additional extra amino acids including proline were incorporated (the hinge regions) and a translation stop codon signal in frame with the fragment C open reading frame.

30

The PCR product was gel-purified and digested with SacII and BamHI, and cloned into the residual 2.8 kb vector pTETnir15 which had previously been digested by SacII and BamHI. The resulting plasmid purified from transformed colonies and named pTECH 1 is shown in Figure 1. Heterologous sequences such as the sequence encoding the Schistosoma mansoni P28 glutathione S-transferase (P28) were cloned into the XbaI SpeI and BamHI sites in accordance with known methods.

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EXAMPLE 2

Construction of pTECH2

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To further improve the utility of pTECH1, a short linker sequence was introduced between the XbaI and BamHI sites in pTECH1 to allow the directional cloning of oligonucleotides and to also facilitate the construction of multiple tandem epitopes, ("repitopes") (Figure 2). Two complementary oligonucleotides were synthesised bearing the restriction enzyme target sites for BamHI, EcoRV, HindIII, SpeI, followed by a translational stop codon (Table 1). The oligonucleotides were tailored with XbaI and BamHI cohesive ends; however, the BamHI target sequence was designed to include a mismatch and, upon cloning, this restriction site in pTECH1 is destroyed. This version of the vector was designated pTECH2.

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EXAMPLE 3

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Construction of pTECH1-P28

A P28 gene expression cassette was produced by PCR using pUC19-P28 DNA (a kind gift from Dr R Pierce, Pasteur Institute, Lille) as template. Oligonucleotide primers were designed to amplify the full length P28 gene beginning

with the start codon and terminating with the stop codon. In addition, the sense and antisense primers were tailored with the restriction sites for XbaI and BamH I respectively. The product was gel-purified and digested with XbaI and BamH I and then cloned into pTECH1 which had previously been digested with these enzymes and subsequently gel-purified.

5

Expression of the TetC-P28 fusion protein

Expression of the TetC-P28 fusion protein was evaluated by SDS-PAGE and Western blotting of bacterial cells harbouring the construct. It was found that the fusion protein remains soluble, cross-reacts with antisera to both TetC and P28, and is also of the expected molecular weight, 80kDa, for a full length fusion.

10

The fusion protein was stably expressed in a number of different genetic backgrounds including E.coli (TG2) and S. typhimurium (SL5338, SL3261) as judged by SDS-PAGE and Western blotting. Of interest was a minor band of 50kDa which co-migrates with the TetC-Hinge protein alone and cross-reacts exclusively with the anti-TetC sera is visible in a Western blot. As the codon selection in the hinge region has been designed to be suboptimal, the rare codons may cause pauses during translation which may occasionally lead to the premature termination of translation, thus accounting for this band.

15

Affinity purification of the TetC-P28 fusion

20

Glutathione is the natural substrate for P28, a glutathione S-transferase. The amino acid residues involved in binding glutathione are thought to be spatially separated in the primary structure of the polypeptide and brought together to form a glutathione binding pocket in the tertiary structure (P. Reinemer *et al.* EMBO, J8, 1997-2005, 1991). In order to gauge whether the P28 component of the fusion has folded correctly to adopt a conformation capable of binding glutathione, its ability to be affinity purified on a glutathione-agarose matrix was tested. The results obtained (not shown) demonstrated that TetC-P28 can indeed bind to the matrix and the binding is reversible, as the fusion can be competitively eluted with free glutathione.

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EXAMPLE 4

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Construction of pTECH2-P28(aa115-131) peptide fusions

Complementary oligonucleotides encoding the aa115-131 peptide were designed with a codon selection for optimal expression in E.coli [H. Grosjean *et al* idem]. The oligonucleotides were tailored with BglII and SpeI cohesive ends which were generated upon annealing and cloned into pTECH2 which had previously been digested with BamH I and SpeI (Figure 3).

35

Repeated tandem copies of the epitopes (reptopes) were constructed in pTECH2 by the following approach. The recombinant fusion vector was digested with XbaI and SpeI and to each digest was added a second restriction enzyme which cuts uniquely elsewhere within the vector, e.g. PstI which makes a cut exclusively within the ampicillin resistance gene (Figure 4). DNA fragments containing the epitope sequences can be purified from each of the double digests, mixed and then ligated. XbaI cleaves its target sequence to generate a 5'-CTAG overhang which is compatible with the SpeI overhang. Upon ligation the recognition sequences of both these enzymes are destroyed. In this way the Xba-SpeI restriction sites remain unique and the procedure can be simply and effectively repeated to construct recombinant fusion vectors expressing four or eight tandem copies of the epitopes (Figure 4). A similar strategy has been used by others in the generation of a multimeric fusion protein for the production of a neuropeptide [T. Kempe *et al.* Gene 39, 239-45, 1985].

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Expression of the TetC-peptide fusion proteins

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Expression of the TetC-peptide fusions as monomeric, dimeric, tetrameric, and octameric tandem peptide repeats was evaluated by SDS-PAGE and Western blotting of the bacterial strains harbouring the constructs. The fusion proteins remain soluble, cross-react with both antisera to TetC and P28, and are also of the expected molecular weight [Figure 5]. Furthermore the fusion proteins are expressed in a number of different genetic backgrounds including E.coli (TG2) and S. typhimurium (SL5338, SL3261) as judged by SDS-PAGE and Western blotting. There appeared to be some degradation of the reptopes consisting of higher numbers of copies, as indicated by the appearance of faint bands of lower molecular weight seen in Western blots probed with the anti-P28 antibody.

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The size of the bands suggested that they consisted of reduced copy number fusions to TetC. As was the case with the TetC-P28 fusion described above, the level of expression of the TetC-peptide fusions was less than that of TetC alone from pTECH2, with the expression level gradually decreasing with increasing copy number.

EXAMPLE 5

Immunological Studies

5 Stability of the plasmid constructs *in vivo* and immunisation of mice

BALB/c mice were given approx. 10^6 cfu *i/v* or 5×10^9 orally of *S. typhimurium* SL3261 and SL3261 harbouring the different constructs. Viable counts on homogenates of liver, spleen and (for orally inoculated mice) lymph nodes performed from days 1-8 (epitope fusions) and 1-11 (vector, octamer and P28 fusions) were similar on media with and without ampicillin, indicating that the plasmids were not being lost during growth in the tissues.

Antibody responses in mice immunised intravenously Antibody responses to the TetC-P28 fusion

Tail bleeds were taken weekly on weeks 3 to 6 from animals from each group of 8 mice. Figure 5 shows that in mice immunised with salmonellae expressing the TetC-P28 fusion, antibody responses to recombinant P28 appeared by week 3, and were positive in 6/6 mice from week 4 onwards. No anti-P28 antibodies were detected in sera from mice immunised with either SL3261 or SL3261-pTETnir15 or pTECH2.

All mice immunised with salmonellae expressing TetC, either alone or as the TetC-P28 fusion (but not with salmonellae alone), made antibody to TetC appearing as early as the third week. (Figure 6).

20 Antibody responses to the TetC-peptide fusions

Mice immunised with salmonellae expressing TetC fused to multiple copies of the aa 115-131 peptide were bled as above and the sera tested by ELISA against the synthetic 115-131 peptide chemically conjugated to ovalbumin, and against recombinant P28. Figure 7 shows that antibody responses to the peptide were detected as early as week 3 and increased thereafter, with responses being stronger to fusions containing greater numbers of copies of the peptide. The octameric fusions elicited the best responses with 4-5 mice positive. No antibody responses were detected against ovalbumin-monomer or recombinant P28 in mice immunised either with SL3261, pTECH2 or the monomeric epitope fusion.

30 Some of the anti-epitope sera recognised the full length P28 protein in ELISA (Figure 5). One mouse injected with the dimeric fusion was positive at week 5, another mouse injected with the tetrameric fusion was positive at week 3. Thereafter sera from at least two mice injected with the octameric fusion consistently recognised P28 from week four up to week six.

In summary the antibody responses against the epitopes improved dramatically with increasing copy number, with the tetrameric and octameric epitope fusions being the most potent. No antibody responses to the monomeric fusion were detected.

Antibody response to TetC in mice immunised with the different fusions

40 The antibody response to TetC was not the same in all groups; the addition of C-terminal fusions to TetC clearly modified the response. Figure 6 shows that the antibody response to TetC elicited by the vector pTECH2 (TetC-Hinge alone) was significantly less than the TetC response to the parental vector, pTETnir15. Surprisingly, the addition to TetC of fusions of increasing size dramatically restores the response to TetC. The anti-TetC response to the largest fusion, full length P28 in pTECH1, was similar to the response to TetC obtained from the parental plasmid (under the conditions tested). Sera from mice injected with non-recombinant SL3261 did not react with TetC at any time during the period tested.

Antibody responses in mice immunised orally

50 Groups of 10 mice were immunised orally with approx. 5×10^9 cfu of SL3261 alone or carrying pTECH1, or pTECH1-P28, given intragastrically in 0.2ml via a gavage tube. Bleeds taken from week 3 to week 10 showed that most mice receiving the recombinant salmonellae made antibody to TetC as early as week 3 (Figure 8). Mice immunised with the TetC-P28 fusion made antibody to P28 which was detectable in approximately half of the mice by week 8, and then declined (Figure 9).

55 Antibody responses in mice immunised with the purified fusion protein

Mice were immunised subcutaneously with affinity purified TetC-P28 fusion protein adsorbed on aluminium hy-

dioxide. Controls received commercial tetanus toxoid alone. Preliminary results indicate that animals given the fusion protein make an antibody response to both TetC and to P28 (data not shown). No anti-P28 antibody was detected in mice given tetanus toxoid.

5 T-cell responses to TetC and P28

Mice were immunised i/v with approximately 10^6 cfu of SL3261, SL3261(pTETnir15) and SL3261(pTECH1-P28). Six months later T-cell responses as IL-2/IL-4 production were measured against salmonella whole cell soluble extract, TetC, recombinant P28 and whole adult worm antigen as described in the section headed Materials and Methods below. 10 Table 2 shows that cells from both groups produced an IL-2/IL-4 response to the sodium hydroxide treated salmonella extract and to TetC. However, cells from mice immunised with the salmonellae expressing the TetC-P28 fusion also responded to both recombinant P28 and whole worm extract.

Thus the salmonella delivery system has elicited both humoral and cellular (T-cell) immune responses to P28.

15 The salmonellae expressing the recombinant antigens all persisted in the mouse tissues as well as the parental strain, and the plasmids were not lost *in vivo*.

Constructs expressing higher molecular weight fusions (full length P28 and octamer) proved to be the most immunogenic. It may be that the immune response has been promoted by the carrier TetC providing additional T-cell helper epitopes [Francis *et al.* Nature 330: 168-170, 1987]. By week 4 all the mice immunised with cells carrying pTECH1-P28 responded to both TetC and also the full length P28 protein following i/v immunisation. Mice immunised orally also responded to TetC and P28, although not all the mice responded to P28. It may well be that the response to P28, could be improved by boosting. Improved constructs consisting of codon optimised hinge regions, codon optimised P28, and multiple copies of full length P28, are currently in preparation.

20 The antibody responses to the epitopes improved dramatically with increasing copy number, with the tetramer and octamer "repitope" fusions displaying the greatest potency.

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EXAMPLE 6

Cloning of HPVE7 protein in pTECH2

30 The full-length HPV type 16 E7 protein gene was cloned into plasmid pTECH2 by an in frame insertion of the gene in the BamHI site of the vector hinge region.

The E7 gene was obtained from plasmid pGEX16E7 (S.A. Comerford *et al.* J Virology, 65, 4681-90 1991). The gene in this plasmid is flanked by two restriction sites: a 3' BamHI site and a 5' EcoRI site. pGEX16E7 DNA was digested with EcoRI and blunt ended by a filling up reaction using Sequenase (DNA polymerase from USB). It was then digested with BamHI to release the 0.3 Kbp full length E7 gene.

35 The gel purified gene was ligated to BamHI-EcoRV double digested pTECH2 and this ligation mixture used to transform competent E.coli HB101 bacteria.

40 Recombinant colonies were selected by colony blotting using two monoclonal antibodies against HPV16 E7 protein as probes, namely 6D and 4F (R.W. Tindle, *et al* J Gen. Vir. 71,1347-54 1990). One of these colonies, named pTE79, was chosen for further analysis.

45 Protein extracts from pTE79 transformed E.coli grown in both aerobic and anaerobic conditions were prepared and analysed by SDS-PAGE and Western blotting. Growth in anaerobic conditions resulted in expression of a recombinant molecule of about 60 KDal which reacted with monoclonal antibodies 6D and 4F and a rabbit polyclonal serum against Tetanus fragment C.

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EXAMPLE 7

Construction of pTECH2-gD

50 An immunologically important antigen from herpes simplex virus type 1 [HSV1] is glycoprotein D, termed gD1 (R. J. Watson *et al* Science 218, 381-383 1982). A truncated gD1 gene cassette, lacking the transmembrane and cytoplasmic domains aa26-340, was synthesised by PCR. The PCR primers used are shown in Table 3. The forward primer was designed to encode the N-terminus of the mature protein and the reverse primer encoded the amino acids immediately 5' to the transmembrane domain. In addition the primers were tailored with BamHI and SpeI restriction sites respectively. The template for the PCR reation was the plasmid pRWFG [a HSV1 gD BamHI-J clone from strain Patton in pBR322; a kind gift from Dr. T. Minson, Cambridge University]. The amplification product was digested with BamHI and SpeI and cloned into pTECH2 which had previously been digested with the respective enzymes.

55 Expression of the TetC-gD1 fusion protein was assessed by SDS-PAGE and Western blotting of bacterial strains

5 harbouring the constructs. The Western blots were probed with either anti-TetC polyclonal sera or a monoclonal antibody directed against amino acids 11-19 of the mature gD [designated LP16, obtained from Dr. T. Minson, Cambridge]. The fusion protein is expressed as a 85kDa band visible on Western blots together with lower molecular weight bands down to 50kDa in size. The lower molecular weight bands could correspond to proteolytic cleavage products of gD or represent the products of premature translational termination within the coding region of gD due to ribosomal pausing. The fusion protein is expressed in the salmonella strains SL5338 and SL3261.

EXAMPLE 8

10 Construction of pTECH2- FMDV/SIV Repitopes

Peptides from the foot and mouth disease virus (FMDV; serotype A12) viral protein [VP1; aa136-159] and the V2 loop from simian immunodeficiency virus [SIV] envelope protein [gp120; aa171-190] were cloned into pTECH2 (M.P. Broekhuijsen *et al* J. Gen. Virol. 68, 3137-45 1987; K.A. Kent *et al* AIDS Res. and Human Retro. 8:1147-1151 1992).

15 Complementary oligonucleotides encoding the peptides were designed with a codon selection for optimal expression in *E. coli* [H. Grosjean *et al* Gene, 18, 199-209, 1982]. The oligonucleotides are shown in Table 3. The oligonucleotides were tailored with BgIII and Spel cohesive ends which were generated upon annealing and cloned into pTECH2 which had previously been digested with BamHI and Spel (Figure 3). Dimeric, tetrameric and octameric fusions of these peptides were constructed as described previously.

20 Expression of the TetC-fusions was assessed by SDS-PAGE and Western blotting with a polyclonal sera directed against TetC and monoclonal antibodies directed against either the FMDV or the SIV epitopes. The FMDV and SIV epitope constructs expressed the TetC fusion proteins in both SL5338 and SL3261.

EXAMPLE 9

25 Construction of pTECH2- gp120-P28 Peptide Heteromers

To explore the possibility of delivering more than one type of epitope from a single molecule of TetC, fusions have been made with the P28 and SIV epitopes to produce a tripartite protein. This form of construction has been facilitated 30 by the modular nature of the vector which allows the assembly of vector modules containing different epitopes. These "heteromers" express either tandem dimers or tetramers of the P28 and SIV epitopes. To investigate the effect of the position of a particular epitope in the TetC-Epitope A-Epitope B fusion on its expression level, stability, and immunogenicity, the converse combinations have also been constructed i.e. TetC-Epitope B-Epitope A, as is shown in Figure 11. "Heteromers" constructed in this way are TetC-P28 dimer-SIV dimer, TetC-SIV dimer-P28 dimer, TetC-P28 35 tetramer-SIV tetramer and TetC-SIV tetramer-P28 tetramer.

Expression of the tripartite fusions were evaluated by SDS-PAGE and Western blotting using the antibody reagents described above. These heteromer constructs are all expressed in the *Salmonella* strains SL5338 and SL3261, but intriguingly the expression level and stability is greater in one dimer-dimer and tetramer-tetramer combination (TetC-gp120-P28) than the converse.

40 EXAMPLE 10

MATERIALS AND METHODS

45 Plasmids, Oligonucleotides, and the Polymerase Chain Reaction

The plasmid pTETnir5 directs the expression of fragment C from tetanus toxin under the control of the nirB promoter [Chatfield *et al*. idem Oxer *et al*. idem] The TetC-hinge fusion vector pTECH1 was constructed from pTETnir5 by the polymerase chain reaction (PCR) described by Mullis *et al*, 1986. PCR was performed using the high-fidelity thermostable DNA polymerase from Pyrococcus furiosus, which possesses an associated 3'-5' exonuclease proofreading activity [K.S. Lundberg *et al* Gene 108: 1-6, 1991]. The amplification reaction was performed according to the manufacturer's instructions (Stratagene).

55 Bacterial Strains

The bacterial strains used were *E.coli* TG2 (recA; [J. Sambrook *et al*. Molecular cloning: a laboratory manual. Cold Spring Harbor, New York, 1989]). *S.typhimurium* SL5338 (galE rmp^A [A. Brown J. Infect. Dis. 155: 86-92, *et al* J. Infect. Dis. 155: 86-92, 1987]) and SL3261 (aroA); [S.K. Hoiseth *et al* Nature 291, 238-9, 1981]. Bacteria were cultured in

either L or YT broth and on L-agar with ampicillin (50 µg/ml) if appropriate. Plasmid DNA prepared in *E.coli* was first modified by transformation into SL5338 to increase the efficiency of electroporation into the SL3261 *aroA* (*r^m*) vaccine. For electroporation, cells growing in mid-log phase were harvested and washed in half the initial culture volume of ice-cold water, 1/10 volume of ice-cold glycerol (10%), and finally the cells were resuspended to a concentration of 10¹⁰ cells/ml in ice-cold glycerol (10%). To a pre-chilled cuvette was added a mix of 60 µl cells and 100 ng of plasmid DNA. The cells were pulsed using the Porator from Invitrogen (settings: voltage=1750 µv, capacitance = 40 µF, resistance = 500). Prewarmed L-broth supplemented with 20 mM glucose was added immediately and the cells grown at 37°C with gentle shaking for 1-1.5 h. The cells were then plated on L-agar plates containing ampicillin and incubated at 37°C for 16 h.

SDS-PAGE and Western Blotting

Expression of the TetC fusions was tested by SDS-PAGE and Western blotting. Cells growing in mid-log phase with antibiotic selection were harvested by centrifugation and the proteins fractionated by 10% SDS-PAGE. The proteins were transferred to a nitrocellulose membrane by electroblotting and reacted with either a polyclonal rabbit antiserum directed against TetC or the full length P28 protein. The blots were then probed with goat anti-rabbit-Ig conjugated to horseradish peroxidase (Dako, UK) and developed with 4-chloro-1-naphthol.

Glutathione-Agarose Affinity Purification

Bacterial cells expressing the TetC full length P28 gene fusion were grown to log phase, chilled on ice, and harvested by centrifugation at 2500Xg for 15 min at 4°C. The cells were resuspended in 1/15th the original volume of ice-cold phosphate buffered saline (PBS) and lysed by sonication in a MSE Soniprep. The insoluble material was removed by centrifugation and to the supernatant was added 1/6 volume of a 50% slurry of pre-swollen glutathione-agarose beads. (Sigma, UK.). After mixing gently at room temperature for 1 h the beads were collected by centrifugation at 1000Xg for 10 sec. The supernatant was discarded and the beads resuspended in 20 volumes of cold PBS-0.5% Triton X-100 and the beads collected again by centrifugation. The washing step was repeated three more times. The fusion protein was eluted by adding 1 volume of 50 mM Tris-HCl, pH 8.0 containing 5.0 mM reduced glutathione (Sigma). After mixing gently for 10 min the beads were pelleted as before and the supernatant removed. The elution step was repeated five more times and the supernatant fractions analysed by SDS-PAGE.

Animals

Female BALB/c mice were purchased from Harlan Olac UK Blackthorn, Bicester, UK, and used when at least 8 weeks of age.

Inoculations and viable counting or organ homogenates

Bacteria were grown in tryptic soy broth (Oxoid) supplemented with 100 µg/ml ampicillin as required. For intravenous inoculation, stationary cultures were diluted in PBS and animals were given approx. 10⁶ cfu in a lateral tail vein in 0.2 ml. For oral inoculation, bacteria were grown in shaken overnight cultures, concentrated by centrifugation, and animals received approximately 5X10⁹ cfu in 0.2 ml intragastrically via a gavage tube. The inoculum doses were checked by viable counts on tryptic soy agar. For viable counts on organ homogenates, groups of 3 mice were sacrificed at intervals, the livers and spleen and (for orally inoculated mice) a pool of mesenteric lymph nodes were homogenised separately in 10 ml distilled water in a Colworth stomacher [C.E. Hormaeche Immunology 37, 311-318, 1979] and viable counts performed on tryptic soy agar supplemented with 100 µg/ml ampicillin.

Measurement of antibody responses

Antibodies were measured by solid phase immunoassay. 96-well-flat bottomed plates were coated with either 0.1 µg of TetC (a kind gift from Dr N Fairweather, the Wellcome Foundation, Beckenham UK) or 1 µg of recombinant P28 (a kind gift from Dr R Pierce, Pasteur Institute, Lille, France) in 100 µl of 0.1 M carbonate buffer, pH 9.6. After overnight incubation at 4°C the plates were incubated for 1 h at 37°C. Blocking of non-specific binding sites was carried out by incubation with 200 µl of 2% casein (BDH, Poole, UK) in PBS pH 7.0 for 1 h at 37°C. Plates were washed three times with 0.05% Tween 20 (Sigma) in PBS with a semiautomatic ELISA washer (Titertek, Flow/ICN, Herts UK). 100 µl of sera from inoculated mice diluted 1:20 in 2% casein was added to each well and the plates were incubated for one hour at 37°C. The plates were washed as above and 100 µl of horse radish peroxidase conjugated goat antimouse immunoglobulins (Dako, Bucks UK), diluted according to the manufacturer's instructions in 2% casein in PBS, was

added to each well and incubated for one hour at 37°C. The plates were washed as above and three more washes were given with PBS alone. The plates were developed using 3,3',3,3'-tetramethylbenzidine dihydrochloride (Sigma) according to the manufacturer's instructions using phosphate/citrate buffer, pH 5.0 and 0.02% hydrogen peroxide. The plates were incubated for 10-15 min at 37°C after which the reaction was stopped with 25 µl 3M H₂SO₄ (BDH). The plates were read in an ELISA reader at 450 nm.

Measurement of T-cell responses

Spleens from mice vaccinated 6 months in advance were removed aseptically and single cell suspensions were prepared by mashing the spleens through a stainless steel sieve with the help of a plastic plunger. Cells were washed once in RPMI1640 medium (Flow/ICN) at 300xg and incubated in Gey's solution to lyse the red cells. White cells were washed twice more as above and resuspended in complete medium, i.e. RPMI1640 supplemented with 100 U/ml penicillin G (Flow/ICN), 100 µg/ml streptomycin (Flow/ICN), 2X10⁻⁵ M B-mercapto-ethanol (Sigma), 1mM N-(2-hydroxyethyl-piperazine-N'-(2-ethanesulphonic acid) (HEPES) (Flow/ICN) and 10% heat inactivated newborn bovine serum (Northumbria Biolabs, Northumberland, UK). For isolation of T-cells, spleen cells were treated as above and after lysis of red cells the white cells were resuspended in warm (37°C) RPMI1640 and passed through a Wigzell glass bead column [H. Wigzell, *et al* Scand. J. Immunol 1: 75-87, 1972].

Cells were plated at 2X10⁶/ml in a final volume of 200 µl of complete medium in 96-well plates in the presence of the relevant antigens. These were either an alkali-treated whole cell soluble extract of *S.typhimurium* C5 prepared as described in Villarreal *et al*. [Microbial Pathogenesis 13: 305-315, 1992] at 20 µg/ml final concentration; TetC at 10 µg/ml; recombinant *Schistosoma mansoni* P28 at 50 µg/ml; and *S.mansoni* whole adult worm extract (a kind gift from Dr D Dunne, Cambridge University) at 20 µg/ml. Cells were incubated in a 95% humidity, 5% CO₂, 37°C atmosphere.

Feeder cells for T-cells for animals immunised with SL3261(pTECH1-P28) were obtained from syngeneic BALB/c naive spleens prepared as above. For mice immunised with pTETnir15, feeder cells were obtained from similarly immunised animals. After red cell lysis and two washes with RPMI1640 cells were X-ray irradiated at 2000 rads and washed twice more. These antigen presenting cells were resuspended in complete medium to give a final ratio of 1:1 with T-cells.

IL-2 production and assay

T-cell suspensions were plated as above. After two days, 50 µl of supernatant was harvested and added to 1x10⁴ cells/well CTLL-2(IL-2 dependent) in 50 µl of medium. CTLL-2 cells were obtained from Dr J Ellis, University College, London UK and maintained in RPMI1640 supplemented as above, substituting the newborn bovine serum for foetal bovine serum. After 20 h, 20 µl of MTT at a concentration of 5 mg/ml in PBS were added. MTT transformation was measured as indicated elsewhere [Tada *et al*. J. Immunol. Methods 93: 157-165, 1986], results were expressed as the mean of the optical density of triplicates read at 570 nm using a reference filter of 630 nm. Significance was determined by Student's t-test.

BACTERIAL SAMPLE DEPOSITS

Salmonella typhimurium strains SL3261-pTECH1, SL3261-pTECH1-P28, SL3261-pTECH2, SL3261-pTECH2-P28 Octamer and PTE79 have been deposited at the National Collection of Type Cultures, 61 Colindale Avenue, London, NW9 5HT, UK, on 15th July 1993 under Deposit Numbers NCTC 12831, NCTC 12833, 12832, 12834 and 12837 respectively.

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TABLE 1**DNA SEQUENCES OF OLIGONUCLEOTIDES UTILISED IN THE CONSTRUCTION OF THE TETC-HINGE VECTORS****A). Primer 1. Sense PCR (21mer). (SEQ ID NO: 4)**

SacII

5'AAA GAC TCC GCG GGC GAA GTT -3'

TETANUS TOXIN C FRAGMENT SEQ.

B). Primer 2. Anti-Sense PCR Primer (64mer). (SEQ ID NO: 5)

BamHI STOP SpeI XbaI HINGE REGION

5'- CTAT GGA TCC TTA ACT AGT GAT TCT AGA GGG CCC CGG CCC

GTC GTT GGT CCA ACC TTC ATC GGT -3'

TETANUS TOXIN C FRAGMENT SEQ. 3'-END

C). The pTECH2 Linker (SEQ ID NO: 6)

XbaI BamHI EcoRV HindIII SpeI Stop XBamHI*

5'-CTAGA GGATCC GATATC AAGCTT ACTAGT TAA T-3'

3'-T CCTAGG CTATAG TTCTGAA TGATCA ATT ACTAG-5'

*This BamHI recognition sequence is now destroyed.

TABLE 2

T-Cell responses (IL-2/IL-4 production) elicited by alkali treated salmonella whole cell extract (C5NaOH), TetC, *Schistosoma mansoni* whole adult worm antigen (SWA), and recombinant P28 in mice immunised with SL3261 (pTETnir15) or SL3261(pTECH1.P28).

| Immunising strain | | CSNaOH | Stimulating antigen | | |
|--------------------|-----|--------|---------------------|-----|-----|
| | | | TetC | P28 | SWA |
| SL3261 (pTETnir15) | 2±4 | 67±5 | 41±1 | 0 | 0 |

TABLE 2 (continued)

5 T-Cell responses (IL-2/IL-4 production) elicited by alkali treated salmonella whole cell extract (C5NaOH), TetC,
Schistosoma mansoni whole adult worm antigen (SWA), and recombinant P28 in mice immunised with SL3261
 (pTETnir15) or SL3261(pTECH1.P28).

| Stimulating antigen | | | | | |
|--|-------|--------|------|--------------|-------------|
| Immunising strain | none | CSNaOH | TetC | P28 | SWA |
| SL3261 (pTECH1-P28) | 6±2.6 | 109±10 | 50±8 | 25±8 p<0.001 | 17±6 p<0.01 |
| Results expressed as (A ₅₇₀ -A ₆₃₀) x 1000±S.D. | | | | | |

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TABLE 3Oligonucleotide Sequences for HSV, FMDV, and SIV.5 HSV1 gD Gene

PCR Primer 1: 5'-AATGGATCCAAATATGCCCTGGCGGATGC-3'
 (SEQ ID NO: 7)

10 PCR Primer 2: 5'-TTAACTAGTGTGTTGGGGTGGCCGGGGAT-3'
 (SEQ ID NO: 8)

FMDV VP1 Epitope

15 Oligo 1:
 5'-GATCTAAATACTCTGCTTCTGGTTCTGGTGTTCGTGGTGAC
 TTCGGTTCTCTGGCTCCGCGTGTGCTCGTCAGCTGA-3'
 (SEQ ID NO: 9)

20 Oligo 2:
 5'-CTAGTCAGCTGACGAGCAACACGCGGAGCCAGAGAACCGAA
 GTCACCACGAACACCAAGAACCGAGAGTATTAA-3
 (SEQ ID NO: 10)

25 SIV gp120 Epitope

Oligo 1:
 5'-GATCTAACATGACCGGTCTGAAACGTGATAAAACCAAAGAA
 TACAACGAAACCTGGTACTCTACCA-3'
 (SEQ ID NO: 11)

Oligo 2:
 5'-CTAGTGGTAGAGTACCAAGGTTCTGTTGATTCTTGGTTT
 ATCACGTTCAGACCGGTATGTTA-3'
 (SEQ ID NO: 12)

Sm P28 Gene

40 PCR Primer 1: 5'-TAGTCTAGAATGGCTGGCGAGCATATCAAG-3'
 (SEQ ID NO: 13)

PCR Primer 2: 5'-TTAGGATCCTAGAAGGGAGTTGCAGGCCT-3'
 (SEQ ID NO: 14)

45 Sm P28 Epitope

Oligo 1:
 5'-GATCTAACCGCAGGAAGAAAAAGAAAAATCACCAAAGAAA
 TCCTGAACGGAAAA-3'
 (SEQ ID NO: 15)

Oligo 2:
 5'-CTAGTTTGCCGTTCAAGGATTCTTGGTGATTTTTCTTTCT
 TCCTGCAGTTA-3'
 (SEQ ID NO: 16)

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:

- (A) NAME: MEDEVA HOLDINGS BV
(B) STREET: CHURCHILL-LAAN 223
(C) CITY: AMSTERDAM
10 (E) COUNTRY: THE NETHERLANDS
(F) POSTAL CODE (ZIP): 1078 ED

15 (ii) TITLE OF INVENTION: VACCINES

17 (iii) NUMBER OF SEQUENCES: 20

(iv) COMPUTER READABLE FORM:

- 20 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

25 (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 9216317.9
(B) FILING DATE: 31-JUL-1992

30 (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 9306398.0
(B) FILING DATE: 26-MAR-1993

(2) INFORMATION FOR SEQ ID NO: 1:

35 (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli

(ix) FEATURE:

- 55 (A) NAME/KEY: promoter
(B) LOCATION: 1..61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AATTCAGGTA AATTGATGT ACATCAAATG GTACCCCTTG CTGAATCGTT AAGGTAGGCCG 60

5 GTAGGGCC 68

(2) INFORMATION FOR SEQ ID NO: 2:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

25 AATTCAGGTA AATTGATGT ACATCAAATG GTACCCCTTG CTGAATCGTT AAGGTAGGCCG 60

GTAGGGCC 68

30 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTACCGCCTA CCTAACGAT TCAGCAAGGG GTACCATTG ATGTACATCA AATTTACCTG 60

50 (2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

10 **AAAGACTCCG CGGGCAGGT T****21**

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25 (iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

30 **CTATGGATCC TAACTAGTG ATTCTAGAGG GCCCCGGCCC GTCGTTGGTC CAACCTTCAT****60****CGGT****64**

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50

CTAGAGGATC CGATATCAAG CTTACTAGTT AAT**33**

55 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

- (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

15 AATGGATCCA AATATGCCCT GGCGGATGC

29

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTIC

(A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

35 TAACTAGTGT TGTTGGGGT GGGCGGGGGA T

21

(2) INFORMATION FOR SEQ ID NO: 9:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATCTAAATA CTCTGCTTCT GGTTCTGGTG TTCTGTGGTGA CTTCTGGTTCT CTGGCTCCCC

60

GTGTTGCTCG TCAGCTGA

70

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15 (v) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

| | |
|---|----|
| CTAGTCAGCT GACGAGCAAC ACGCGGAGCC AGAGAACCGA AGTCACCACG AACACCAGAA | 60 |
| 20 CCAGAACGAG AGTATTAA | 78 |

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (v) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

| | |
|--|----|
| 40 GATCTAACAT GACCGGTCTG AAACGTGATA AAACCAAAGA ATACAACGAA ACCTGGTACT | 60 |
| CTACCA | 66 |

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTAGTGGTAG AGTACCAGGT TTCGTTGTAT TCTTTGGTTT TATCACGTTT CAGACCGGTC 60
ATGTTA 66

(2) INFORMATION FOR SEQ ID NO: 13:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

25 TAGTCTAGAA TGGCTGGCGA GCATATCAAG

30

(2) INFORMATION FOR SEQ ID NO: 14:

30 (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40

AN ALGEBRAIC APPROACH TO THE ANALYSIS OF SPATIAL MODELS 11

45 TTGCCCTGCT TCGAAGCCAG TTGGACCCCT

28

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

GATCTAAACC GCAGGAAGAA AAAGAAAAAA TCACCAAAGA AATCCTGAAC GGCAAAA

57

10 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CTAGTTTGC CGTTCAGGAT TTCTTGGTG ATTTTTCTT TTCTTCCTG CGGTTTA

57

30 (2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCAGGTAAA TTTGATGTAC ATCAAATGGT ACCCCCTTGCT GAATCGTTAA GGTAGGGCGGT

60

50 AGGGGCCAGA TCTTAATCAT CCACAGGAGA CTTTCTGATG AAAAAACCTTG ATTGTTGGGT

120

| | | |
|----|--|------|
| | CGACAAACGAA GAAGACATCG ATGTTATCCT GAAAAAGTCT ACCATTCTGA ACTTGGACAT | 180 |
| 5 | CAACAAACGAT ATTATCTCCG ACATCTCTGG TTTCAACTCC TCTGTTATCA CATATCCAGA | 240 |
| | TGCTCAATTG GTGCCGGGCA TCAACGGCAA AGCTATCCAC CTGGTTAACCA ACGAATCTTC | 300 |
| 10 | TGAAGTTATC GTGCACAAGG CCATGGACAT CGAATAACAC GACATGTTCA ACAACTTCAC | 360 |
| | CGTTAGCTTC TGGCTGCGCG TTCCGAAAGT TTCTGCTTCC CACCTGGAAC AGTACGGCAC | 420 |
| 15 | TAACGAGTAC TCCATCATCA GCTCTATGAA GAAACACTCC CTGTCCATCG GCTCTGGTTG | 480 |
| | GTCTGTTCC CTGAAGGGTA ACAACCTGAT CTGGACTCTG AAAGACTCCG CGGGCGAAGT | 540 |
| 20 | TCGTCAGATC ACTTTCCGCG ACCTGCCGGA CAAGTTCAAC GCGTACCTGG CTAACAAATG | 600 |
| | GGTTTCATC ACTATCACTA ACGATCGTCT GTCTTCTGCT AACCTGTACA TCAACGGCGT | 660 |
| 25 | TCTGATGGGC TCCGCTGAAA TCACTGGTCT GGGCGCTATC CGTGAGGACA ACAACATCAC | 720 |
| | TCTTAAGCTG GACCGTTGCA ACAACAACAA CCAGTACGTA TCCATCGACA AGTTCCGTAT | 780 |
| 30 | CTTCTGAAA GCACTGAACC CGAAAGAGAT CGAAAAACTG TATACCAGCT ACCTGTCTAT | 840 |
| | CACCTCCTG CGTGACTTCT GGGGTAACCC GCTGCGTTAC GACACCGAAT ATTACCTGAT | 900 |
| 35 | CCCGGTAGCT TCTAGCTCTA AAGACGTTCA GCTGAAAAAC ATCACTGACT ACATGTACCT | 960 |
| | GACCAACGCG CCGTCCTACA CTAACGGTAA ACTGAACATC TACTACCGAC GTCTGTACAA | 1020 |
| 40 | CGGCCTGAAA TTCATCATCA AACGCTACAC TCCGAACAAC GAAATCGATT CTTCGTTAA | 1080 |
| | ATCTGGTGAC TTCATCAAAC TGTACGTTTC TTACAACAAC AACGAACACA TCGTTGGTTA | 1140 |
| 45 | CCCGAAAGAC GGTAACGCTT TCAACAAACCT GGACAGAATT CTGCGTGTG GTTACAACGC | 1200 |
| | TCCGGGTATC CCGCTGTACA AAAAAATGGA AGCTGTTAAA CTGCGTGACC TGAAAACCTA | 1260 |
| 50 | CTCTGTTCACTGAAACCTGT ACGACGACAA AAACGCTTCT CTGGGTCTGG TTGGTACCCA | 1320 |
| | CAACGGTCAG ATCGGTAACG ACCCGAACCG TGACATCCTG ATCGCTTCTA ACTGGTACTT | 1380 |
| 55 | CAACCACCTG AAAGACAAAAA TCCTGGGTTG CGACTGGTAC TTGCGTCCGA CCGATGAAGG | 1440 |
| | TTGGACCAAC GACGGGCCGG GGCCCTCTAG AATCACTAGT TAAGGATCCG CTAGCCCGCC | 1500 |
| | TAATGAGCGG GCTTTTTTTT CTCGGGCAGC GTTGGGTCTT GGCCACGGGT GCCCATGATC | 1560 |
| | GTGCTCCTGT CGTTGAGGAC CCGGCTAGGC TGGCGGGGTT GCCTTACTGG TTAGCAGAAT | 1620 |
| | GAATCACCGA TACGCGAGCG AACGTGAAGC GACTGCTGCT GCAAAACGTC TGCGACCTGA | 1680 |
| | GCAACAAACAT GAATGGTCTT CGGTTCCGT GTTTCGAAA GTCTGGAAAC GCGGAAGTCA | 1740 |
| | GCGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG GTGCGTCCGC TGCGGCCGAGC | 1800 |

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|----|--|------|
| | GGTATCAGCT CACTCAAAGG CGGTAATAACG GTTATCCACA GAATCAGGGG ATAACGCAGG | 1860 |
| 5 | AAAGAACATG TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAGG CCGCGTTGCT | 1920 |
| | GGCGTTTTTC CATAGGCTCC GCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA | 1980 |
| | GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT | 2040 |
| 10 | CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCCT TTCTCCCTTC | 2100 |
| | GGGAAGCGTG GCGCTTTCTC AATGCTCACG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT | 2160 |
| | TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCCTTCAG CCCGACCGCT GCGCCTTATC | 2220 |
| 15 | CGGTAACATAT CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATGCCAC TGGCAGCAGC | 2280 |
| | CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG | 2340 |
| 20 | GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTGCCCTC TGCTGAAGCC | 2400 |
| | AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG | 2460 |
| | CGGTGGTTTT TTTGTTGCA AGCAGCAGAT TACGCGCAGA AAAAAGGAT CTCAAGAAGA | 2520 |
| 25 | TCCTTGATC TTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT | 2580 |
| | TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG | 2640 |
| 30 | TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT | 2700 |
| | CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTCGTTCA TCCATAGTTG CCTGACTCCC | 2760 |
| | CGTCGTGTAG ATAACCTACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT | 2820 |
| 35 | ACCGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG | 2880 |
| | GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG | 2940 |
| 40 | CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTG CGAACGTTG TTGCCATTGC | 3000 |
| | TGCAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTCAAGCT CCGGTTCCCA | 3060 |
| | ACGATCAAGG CGAGTTACAT GATCCCCAT GTTGTGAAA AAAGCGGTTA GCTCCTTCGG | 3120 |
| 45 | TCCTCCGATC GTTGTCAAA GTAAGTTGGC CGCAGTGTAA TCACTCATGG TTATGGCAGC | 3180 |
| | ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA | 3240 |
| 50 | CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC | 3300 |
| | AACACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG | 3360 |
| | TTCTTCGGGG CGAAAACCTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC | 3420 |
| 55 | CACTCGTGCA CCCAACTGAT CTTCAGCATC TTTTACTTTT ACCAGCGTTT CTGGGTGAGC | 3480 |

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|--|------|
| AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGGATAAGG GCGACACGGA AATGTTGAAT | 3540 |
| ACTCTACTC TTCTTTTC AATATTATTG AAGCATTAT CAGGGTATT GTCTCATGAG | 3600 |
| CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC GCACATTCC | 3660 |
| CCGAAAAGTG CCACCTGACG TCTAAGAAC CATTATTATC ATGACATTA CCTATAAAA | 3720 |
| TAGGCATATC ACGAGGCCCT TTCGTCTCA AGAA | 3754 |

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi)SEQUENCEDESCRIPTION:SEQ ID NO: 18:

| | |
|--|-----|
| TTCAGGTAAA TTTGATGTAC ATCAAATGGT ACCCTTGCT GAATCGTAA GGTAGGCGGT | 60 |
| AGGGCCCAGA TCTTAATCAT CCACAGGAGA CTTCTGATG AAAAACCTTG ATTGTTGGGT | 120 |
| CGACAACGAA GAAGACATCG ATGTTATCCT GAAAAAGTCT ACCATTCTGA ACTTGGACAT | 180 |
| CAACAACGAT ATTATCTCCG ACATCTCTGG TTTCAACTCC TCTGTTATCA CATATCCAGA | 240 |
| TGCTCAATTG GTGCCGGGCA TCAACGGCAA AGCTATCCAC CTGGTTAACCA CGGAATCTTC | 300 |
| TGAAGTTATC GTGCACAAGG CCATGGACAT CGAATACAAC GACATGTTCA ACAACTTCAC | 360 |
| CGTTAGCTTC TGGCTGCGCG TTCCGAAAGT TTCTGCTTCC CACCTGGAAC AGTACGGCAC | 420 |
| TAACGAGTAC TCCATCATCA GCTCTATGAA GAAACACTCC CTGTCCATCG GCTCTGGTTG | 480 |
| GTCTGTTCC CTGAAGGGTA ACAACCTGAT CTGGACTCTG AAAGACTCCG CGGGCGAAGT | 540 |
| TCGTCAGATC ACTTTCCGCG ACCTGCCGGA CAAGTTAAC CCGTACCTGG CTAACAAATG | 600 |
| GGTTTTCATC ACTATCACTA ACGATCGTCT GTCTTCTGCT AACCTGTACA TCAACGGCGT | 660 |
| TCTGATGGGC TCCGCTGAAA TCACTGGTCT GGGCGCTATC CGTGAGGACA ACAACATCAC | 720 |
| TCTTAAGCTG GACCGTTGCA ACAACAACAA CCAGTACGTA TCCATCGACA AGTTCCGTAT | 780 |
| CTTCTGCAAA GCAGTGAACC CGAAAGAGAT CGAAAAACTG TATACCAGCT ACCTGTCTAT | 840 |

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|----|---|------|
| | CACCTTCCTG CGTGACTTCT GGGGTAACCC GCTGCCTTAC GACACCGAAT ATTACCTGAT | 900 |
| 5 | CCC GG TAG CT TCT AG C TCA A AG AC GT TCA G CT G AAA AAC AT CA CT G ACT AC AT GT AC CCT | 960 |
| | GACCAACGCG CCGTCCTACA CTAACGGTAA ACTGAACATC TACTACCGAC GTCTGTACAA | 1020 |
| | CGGCCTGAAA TTCATCATCA AACGCTACAC TCCGAACAAC GAAATCGATT CTTTCGTTAA | 1080 |
| 10 | ATCTGGTGAC TTCATCAAAC TGTACGTTTC TTACAACAAC AACGAACACA TCGTTGGTTA | 1140 |
| | CCCGAAAGAC GGTAACGCTT TCAACAAACCT GGACAGAATT CTGCGTGTG GTTACAACGC | 1200 |
| | TCCGGGTATC CCGCTGTACA AAAAAATGGA AGCTGTTAAA CTGCGTGACC TGAAAACCTA | 1260 |
| 15 | CTCTGTTCAAG CTGAAACTGT ACGACGACAA AAACGCTTCT CTGGGTCTGG TTGGTACCCA | 1320 |
| | CAACGGTCAG ATCGGTAACG ACCCGAACCG TGACATCCTG ATCGCTTCTA ACTGGTACTT | 1380 |
| 20 | CAACCACCTG AAAGACAAAAA TCCTGGGTG CGACTGGTAC TTCGTTCCGA CCGATGAAGG | 1440 |
| | TTGGACCAAC GACGGGCCGG GGCCCTCTAG AGGATCCGAT ATCAAGCTTA CTAGTTAATG | 1500 |
| | ATCCGCTAGC CCGCCTAATG AGCGGGCTTT TTTTCTCGG GCAGCGTTGG GTCCTGGCCA | 1560 |
| 25 | CGGGTGC GCA TGATCGT GCT CCTGTCGTTG AGGACCCGGC TAGGCTGGCG GGGTTGCCTT | 1620 |
| | ACTGGTTAGC AGAATGAATC ACCGATAACGC GAGCGAACGT GAAGCGACTG CTGCTGCAA | 1680 |
| 30 | ACGTCTGCGA CCTGAGCAAC AACATGAATG GTCTTCGGTT TCCGTGTTTC GTAAAGTCTG | 1740 |
| | GAAACGCGGA AGTCAGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT | 1800 |
| | TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGT A TACGGTTAT CCACAGAAC | 1860 |
| 35 | AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA | 1920 |
| | AAAGGCCCGC TTGCTGGCGT TTTTCCATAG GCTCCGCCCG CCTGACGAGC ATCACAAAAA | 1980 |
| 40 | TCGACGCTCA AGTCAGAGGT GGC GAAACCC GACAGGACTA TAAAGATAACC AGGC GTTTCC | 2040 |
| | CCCTGGAAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCCTG CCGCTTACCG GATA CCTGTC | 2100 |
| | CGCCTTCTC CCTTCGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA GGTATCTCAG | 2160 |
| 45 | TTCGGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA | 2220 |
| | CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC | 2280 |
| 50 | GCCACTGGCA GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC | 2340 |
| | AGAGTTCTG AAGTGGTGGC CTA ACTACGG CTACACTAGA AGGACAGTAT TTGGTATCTG | 2400 |
| | CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA | 2460 |
| 55 | AACCACCGCT GGTAGCGGTG GTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA | 2520 |

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|----|--|------|
| | AGGATCTCAA GAAGATCCTT TGATTTTC TACGGGTCT GACGCTCAGT GGAACGAAAA | 2580 |
| 5 | CTCACGTTAA GGGATTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT | 2640 |
| | AAATTAAAAA TGAAGTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG | 2700 |
| 10 | TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC GTTCATCCAT | 2760 |
| | AGTTGCCTGA CTCCCCGTG TGAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC | 2820 |
| 15 | CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA | 2880 |
| | CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCCGTGCA ACTTTATCCG CCTCCATCCA | 2940 |
| 20 | GTCTATTAAT TGGTGCAGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTGCGCAA | 3000 |
| | CGTTGTTGCC ATTGCTGCAG GCATCGTGGT GTCACGCTCG TCGTTGGTA TGGCTTCATT | 3060 |
| 25 | CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT GCAAAAAAGC | 3120 |
| | GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT | 3180 |
| 30 | CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC | 3240 |
| | TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG | 3300 |
| 35 | CTCTTGCCTCG GCGTCAACAC GGGATAATAC CGCGCCACAT AGCAGAACTT TAAAAGTGCT | 3360 |
| | CATCATTGGA AACGTTCTT CGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTTGAGATC | 3420 |
| 40 | CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATTTTTA CTTTCACCAG | 3480 |
| | CGTTTCTGGG TGAGCAAAAA CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC | 3540 |
| 45 | ACGGAAATGT TGAATACTCA TACTCTTCCT TTTCAATAT TATTGAAGCA TTTATCAGGG | 3600 |
| | TTATTGTCTC ATGAGCGGAT ACATATTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT | 3660 |
| 50 | TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA GAAACCATTAA TTATCATGAC | 3720 |
| | ATTAACCTAT AAAAATAGGC GTATCACGAG GCCCTTCGT CTTCAAGAA | 3769 |

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

5 **TCTAGAGGAT CCGATATCAA GCTTACTAGT TAATGATC****38**

(2) INFORMATION FOR SEQ ID NO: 20:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: circular

15 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Gly | Pro | Ser | Arg | Gly | Ser | Asp | Ile | Lys | Leu | Thr | Ser |
| 1 | | | | | 5 | | | | 10 | | | | |

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Claims

1. A vaccine composition comprising a pharmaceutically acceptable carrier and an attenuated bacterium containing a DNA construct comprising a promoter which is capable of promoting expression of a sequence under, and has activity which is induced under, anaerobic conditions, the promoter being operably linked to a DNA sequence encoding first and second proteins linked by a chain of amino acids defining a hinge region.
2. A vaccine composition according to claim 1 wherein the promoter is the nirB promoter or a part or derivative thereof which is capable of promoting expression of a sequence under anaerobic conditions.
3. A vaccine composition according to claim 1 or claim 2 wherein the hinge region comprises proline and/or glycine amino acids.
4. A vaccine composition according to any one of the preceding claims wherein the first protein is an antigenic sequence comprising tetanus toxin C fragment or epitopes thereof.
5. A vaccine composition according to any one of the preceding claims wherein the second protein is an antigenic determinant of a pathogenic microorganism.
6. A vaccine composition according to claim 5 wherein the antigenic determinant is an antigenic sequence derived from a virus, bacterium, fungus, yeast or parasite.
7. A vaccine composition according to claim 6 wherein the antigenic sequence is derived from the P28 protein of Schistosoma mansoni.
8. A vaccine composition according to claim 6 wherein the antigenic sequence is derived from human papilloma virus (HPV).
9. A vaccine composition according to claim 6 wherein the antigenic sequence is derived from herpes simplex virus.
10. A vaccine composition according to claims 6 wherein the antigenic sequence is derived from Foot-and-Mouth virus (FMDV).

11. A vaccine composition according to any one of the preceding claims wherein the attenuated bacterium is selected from the genus Salmonella.

5 Patentansprüche

1. Impfstoffzusammensetzung, umfassend einen pharmazeutisch annehmbaren Träger und ein attenuiertes Bakterium, enthaltend ein DNA-Konstrukt, das einen Promotor umfaßt, der in der Lage ist, die Expression einer Sequenz unter anaeroben Bedingungen zu fördern und Aktivität aufweist, die unter anaeroben Bedingungen induziert wird, wobei der Promoter funktionstüchtig mit einer DNA-Sequenz verknüpft ist, die für erste und zweite Proteine codiert, welche verknüpft sind durch eine Kette von Aminosäuren, die eine Gelenkregion definiert.
2. Impfstoffzusammensetzung gemäß Anspruch 1, wobei der Promotor der nirB-Promotor oder ein Teil oder ein Derivat davon ist, der in der Lage ist, die Expression einer Sequenz unter anaeroben Bedingungen zu fördern.
3. Impfstoffzusammensetzung gemäß Anspruch 1 oder Anspruch 2, wobei die Gelenkregion Prolin- und/oder Glycin-Aminosäuren umfaßt.
4. Impfstoffzusammensetzung gemäß irgendeinem der vorstehenden Ansprüche, wobei das erste Protein eine antigene Sequenz ist, welche ein Tetanus-Toxin-C-Fragment oder Epitope davon umfaßt.
5. Impfstoffzusammensetzung gemäß irgendeinem der vorstehenden Ansprüche, wobei das zweite Protein eine antigene Determinante eines pathogenen Mikroorganismus ist.
6. Impfstoffzusammensetzung gemäß Anspruch 5, wobei die antigene Determinante eine antigene Sequenz, abgeleitet aus einem Virus, Bakterium, Pilz, Hefe oder Parasiten, ist.
7. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz von dem P28-Protein von Schistosoma mansoni abgeleitet ist.
8. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz aus humanem Papillomvirus (HPV) abgeleitet ist.
9. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz aus Herpes Simplex-Virus abgeleitet ist.
10. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz aus Maul-und-Klauenseuchen-Virus (FMDV) abgeleitet ist.
11. Impfstoffzusammensetzung gemäß irgendeinem der vorstehenden Ansprüche, wobei das attenuierte Bakterium aus der Gattung Salmonella gewählt ist.

45 Revendications

1. Une composition de vaccin comprenant un véhicule pharmaceutiquement acceptable et une bactérie atténuee contenant une construction d'ADN comprenant un promoteur qui est capable de promouvoir l'expression d'une séquence, et à une activité qui est induite dans des conditions anaérobies, le promoteur étant lié de manière fonctionnelle à une séquence d'ADN codant pour une première et une seconde protéine liées par une chaîne d'acides aminés définissant une région charnière.
2. Une composition de vaccin selon la revendication 1 dans laquelle le promoteur est le promoteur nirB ou une partie ou un dérivé de celui-ci qui est capable de promouvoir l'expression d'une séquence dans des conditions anaérobies.
3. Une composition de vaccin selon la revendication 1 ou la revendication 2 dans laquelle la région charnière comprend des acides aminés proline et/ou glycine.

4. Une composition de vaccin selon l'une quelconque des revendications précédentes dans laquelle la première protéine est une séquence antigénique comprenant le fragment C de la toxine du tétranos ou des épitopes de celui-ci.
5. Une composition de vaccin selon l'une quelconque des revendications précédentes dans laquelle la seconde protéine est un déterminant antigénique d'un micro-organisme pathogène.
6. Une composition de vaccin selon la revendication 5 dans laquelle le déterminant antigénique est une séquence antigénique provenant d'un virus, d'une bactérie, d'un champignon, d'une levure ou d'un parasite.
- 10 7. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient de la protéine P28 de Schistosoma mansoni.
- 15 8. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient du papillomavirus humain (HPV).
9. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient du virus Herpes simplex.
- 20 10. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient de l'aphtovirus (FMDV).
11. Une composition de vaccin selon l'une quelconque des revendications précédentes dans laquelle la bactérie atténuee est choisie dans le genre Salmonella.

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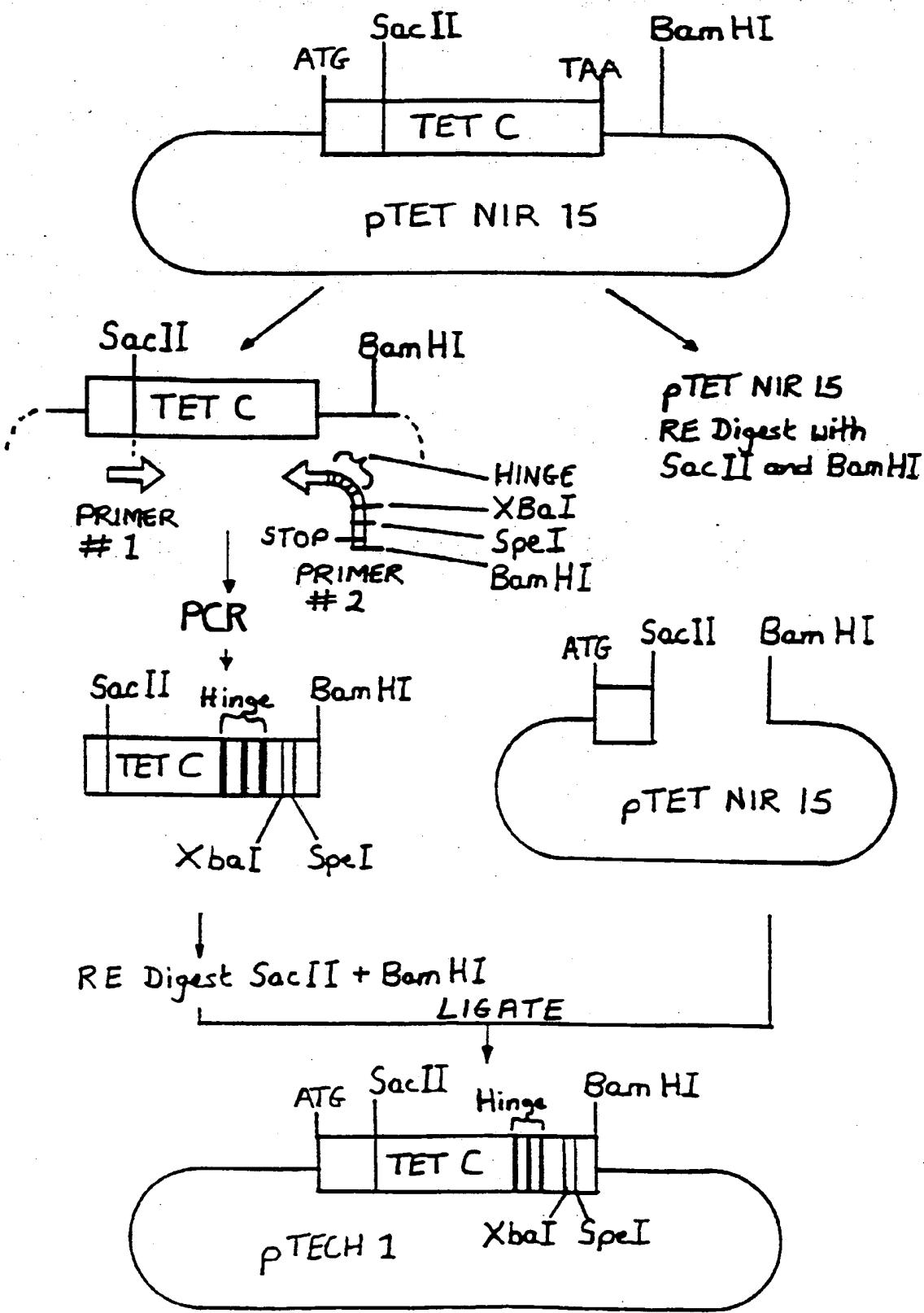


FIGURE 1

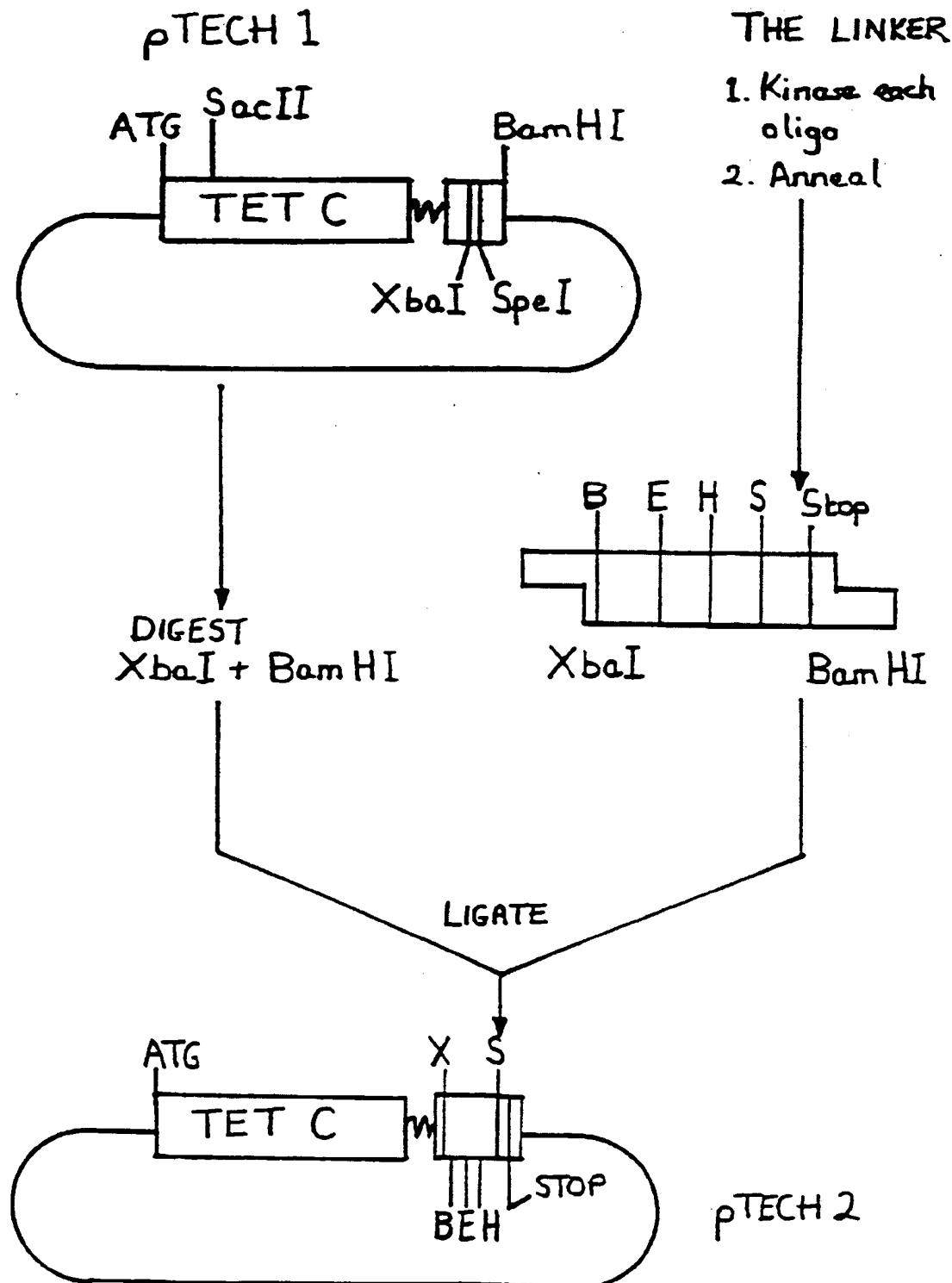


FIGURE 2

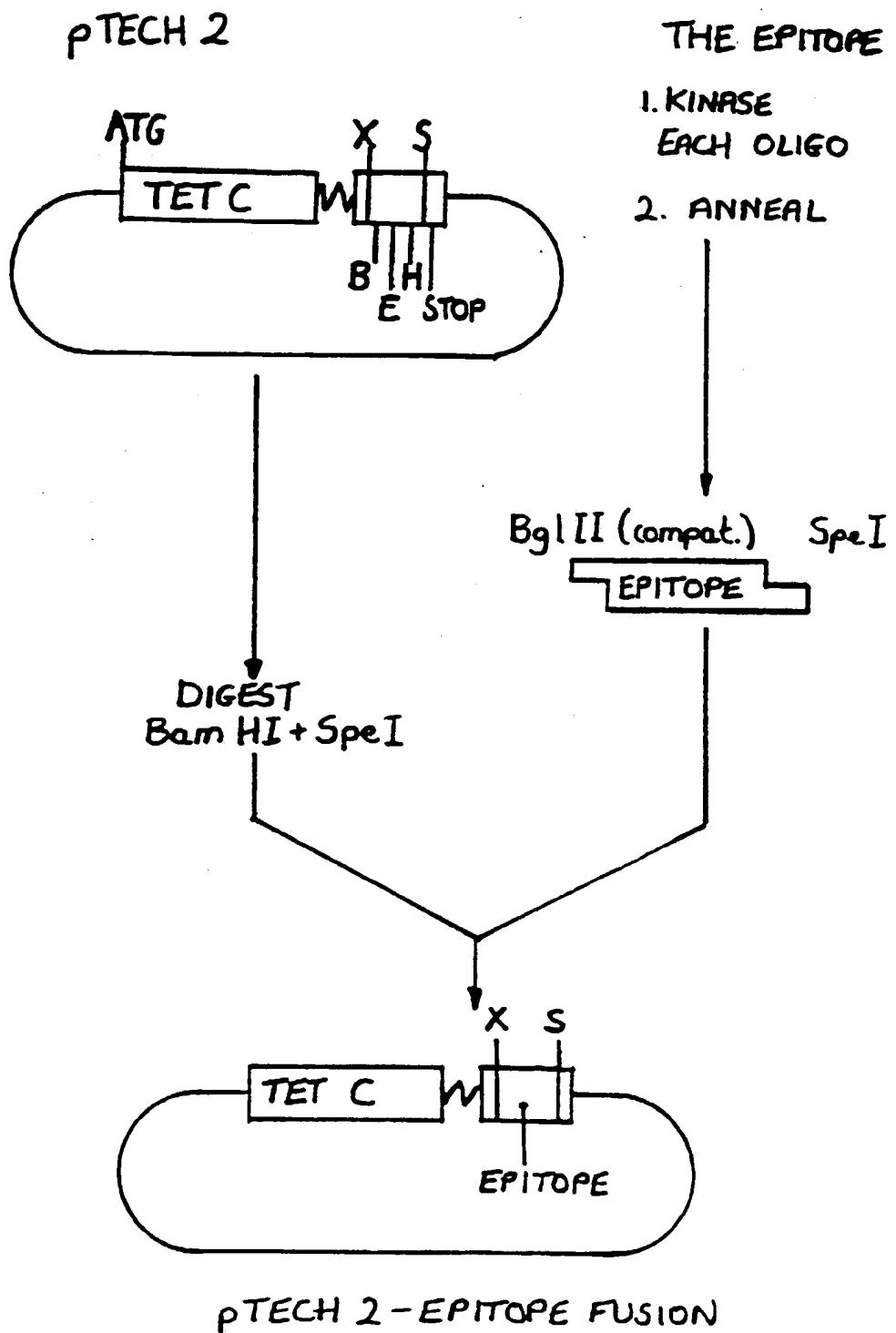


FIGURE 3

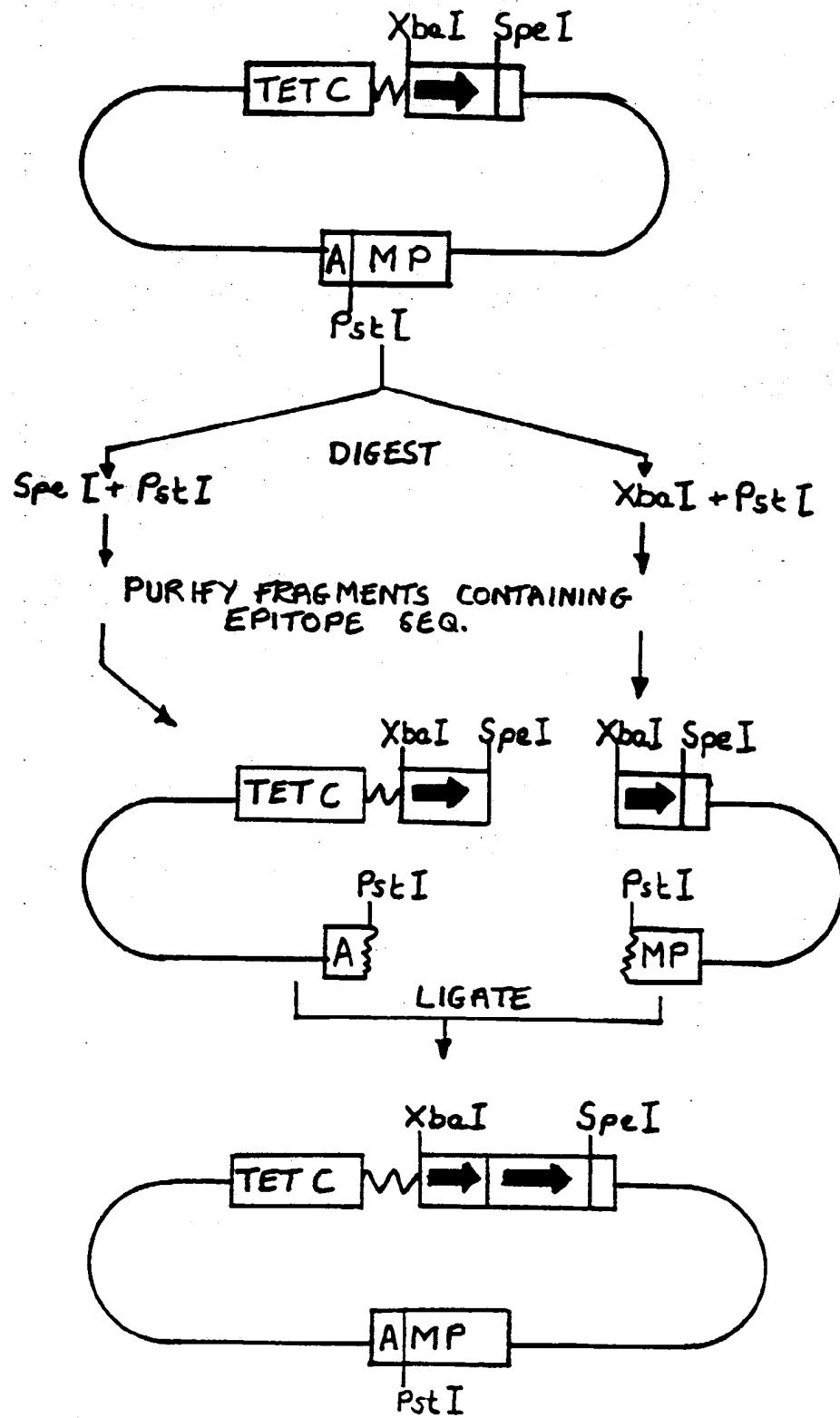
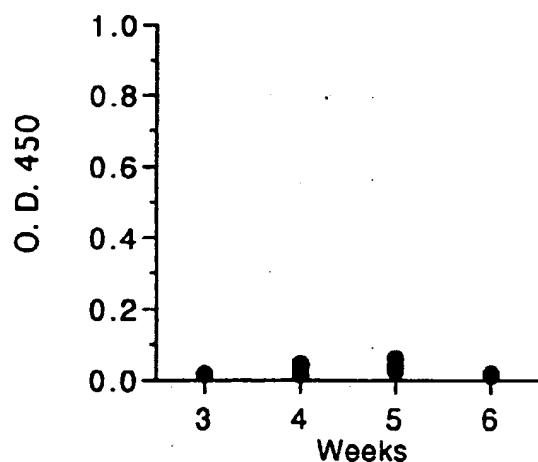
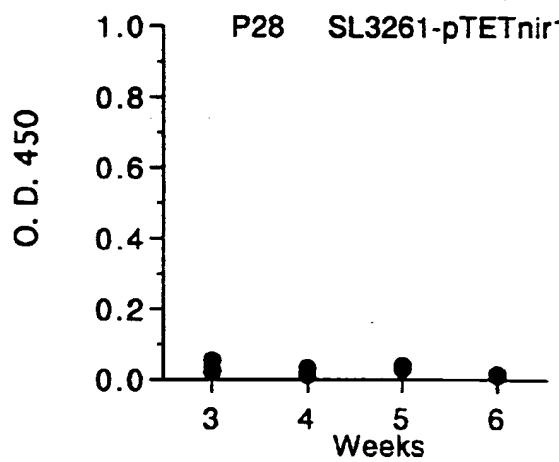


FIGURE 4

P28 SL3261



P28 SL3261-pTETnir15



P28 pTECH2

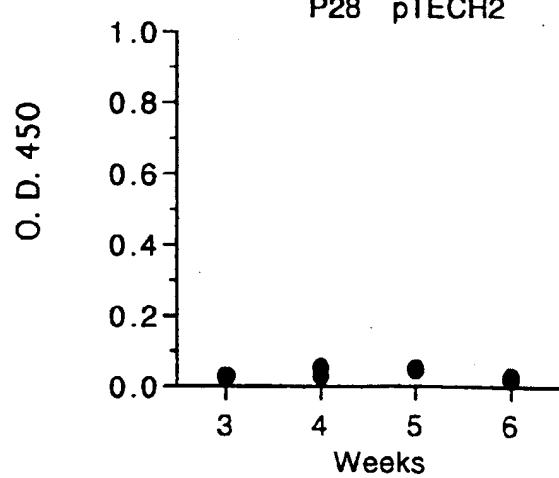


Figure 5

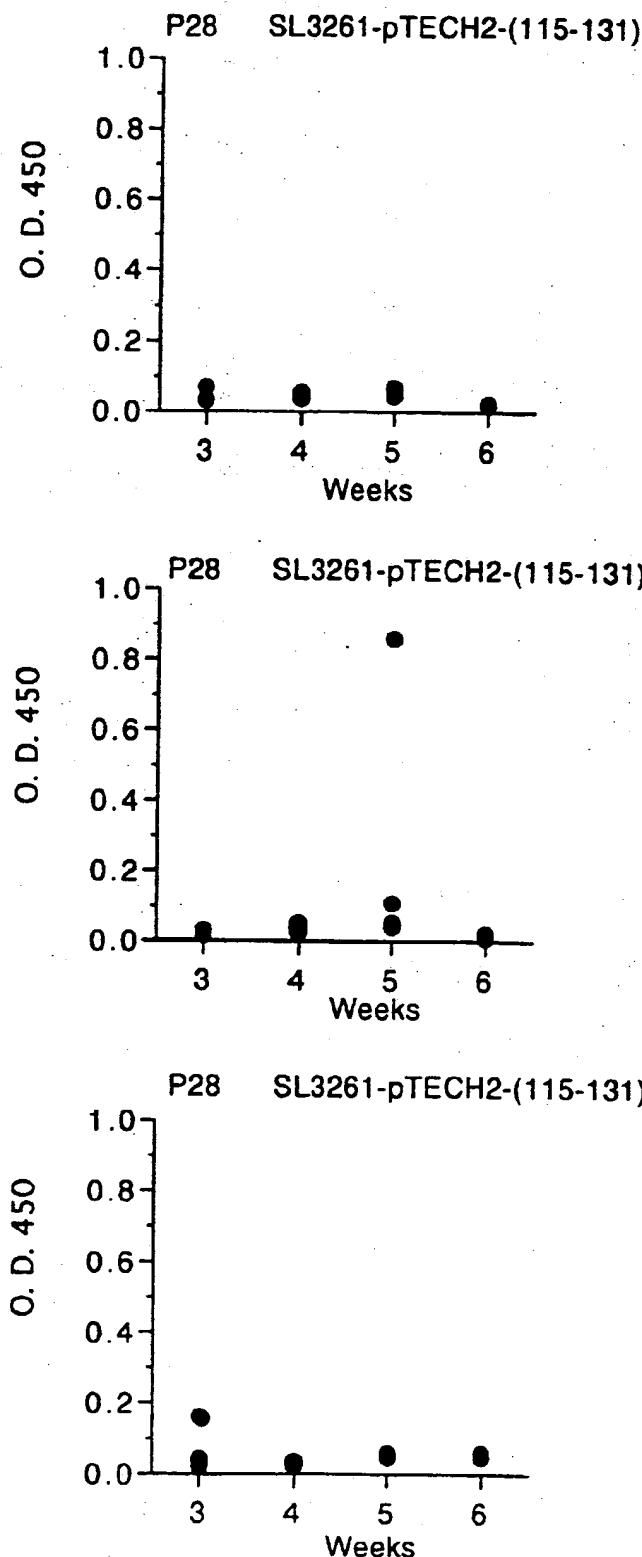


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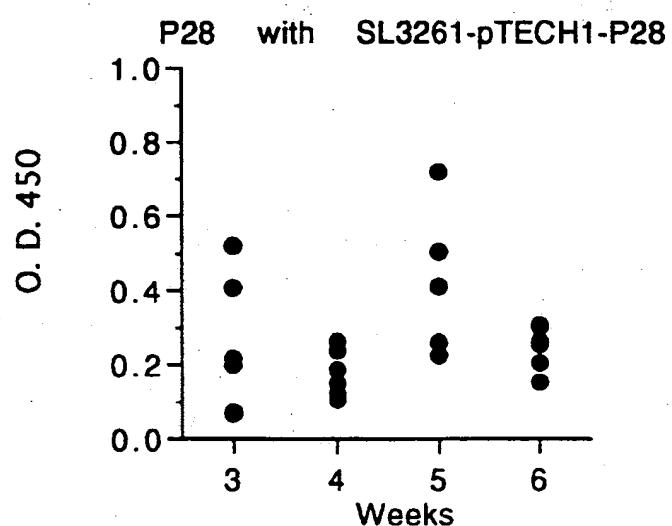
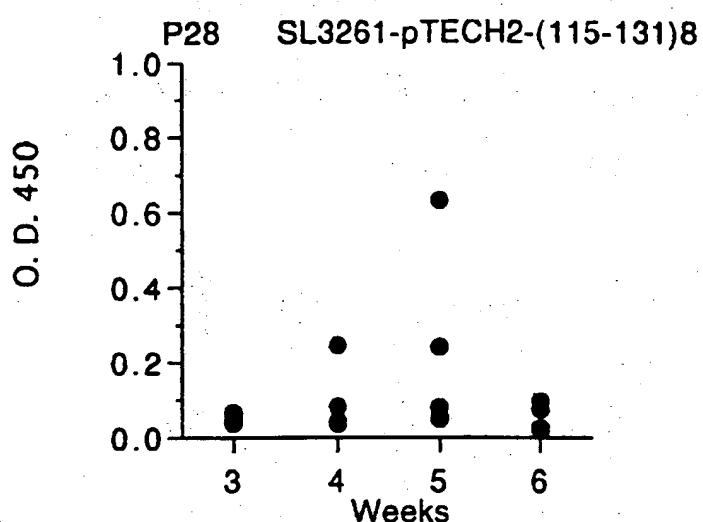


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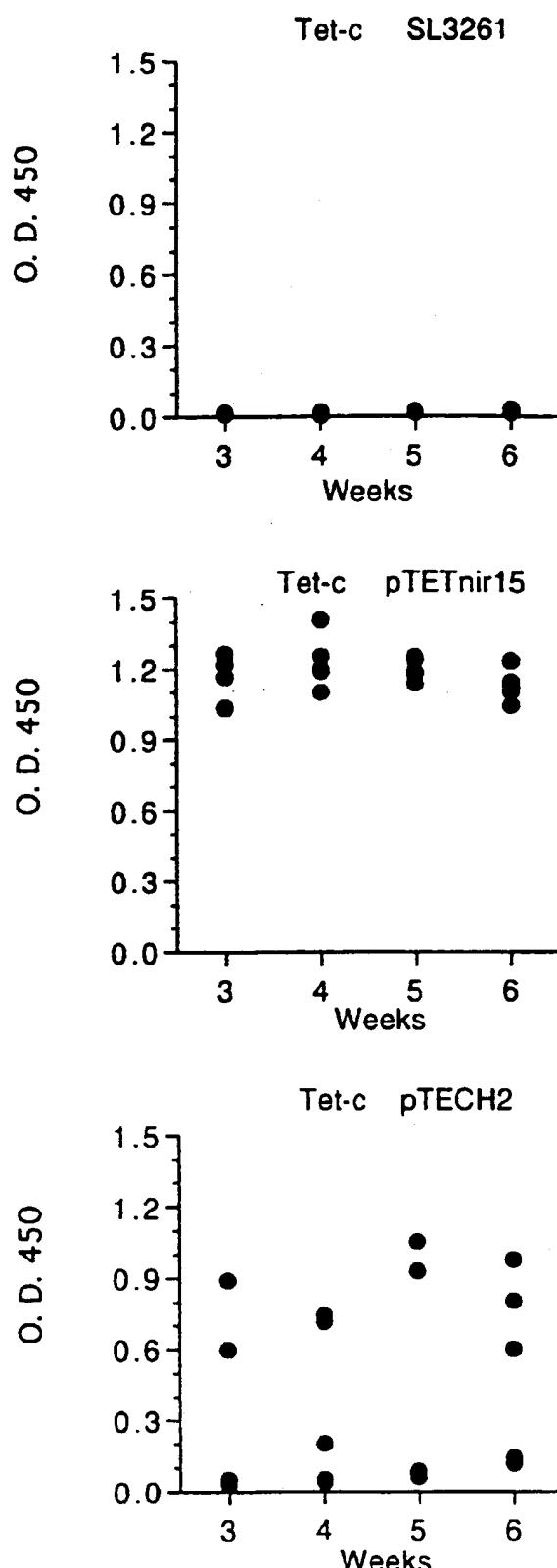


Figure 6

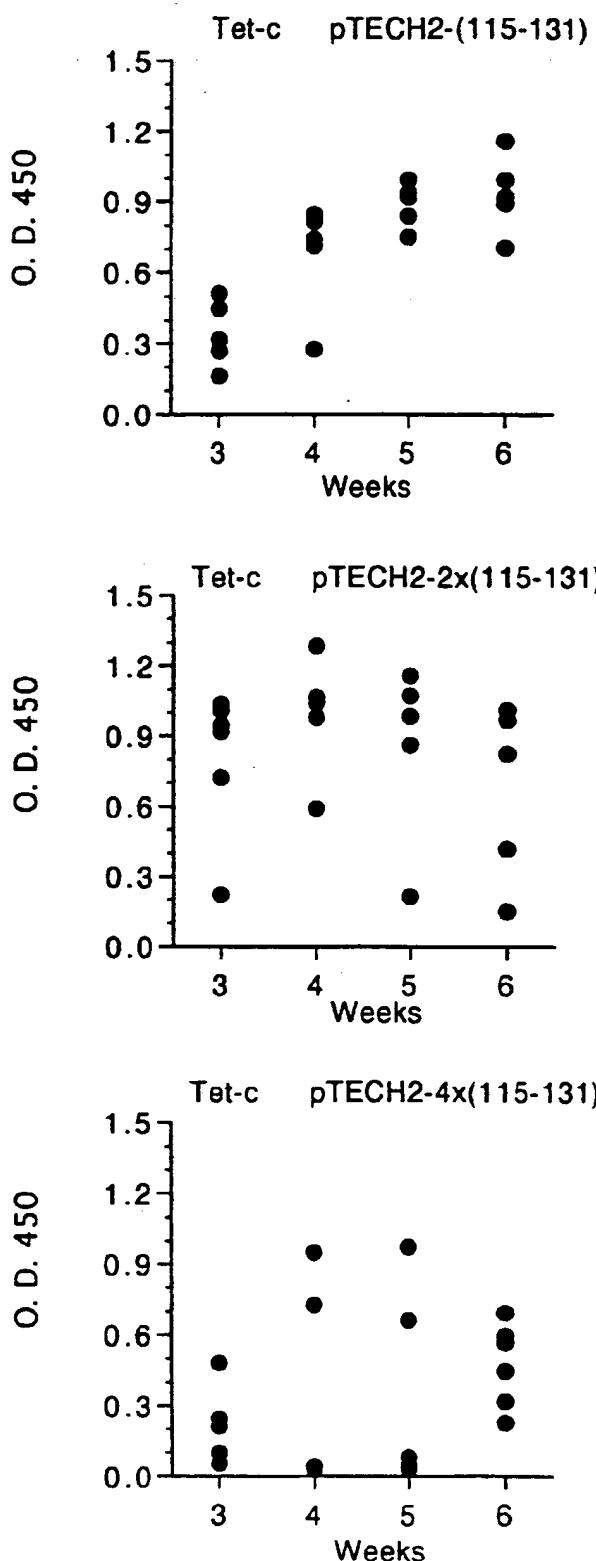


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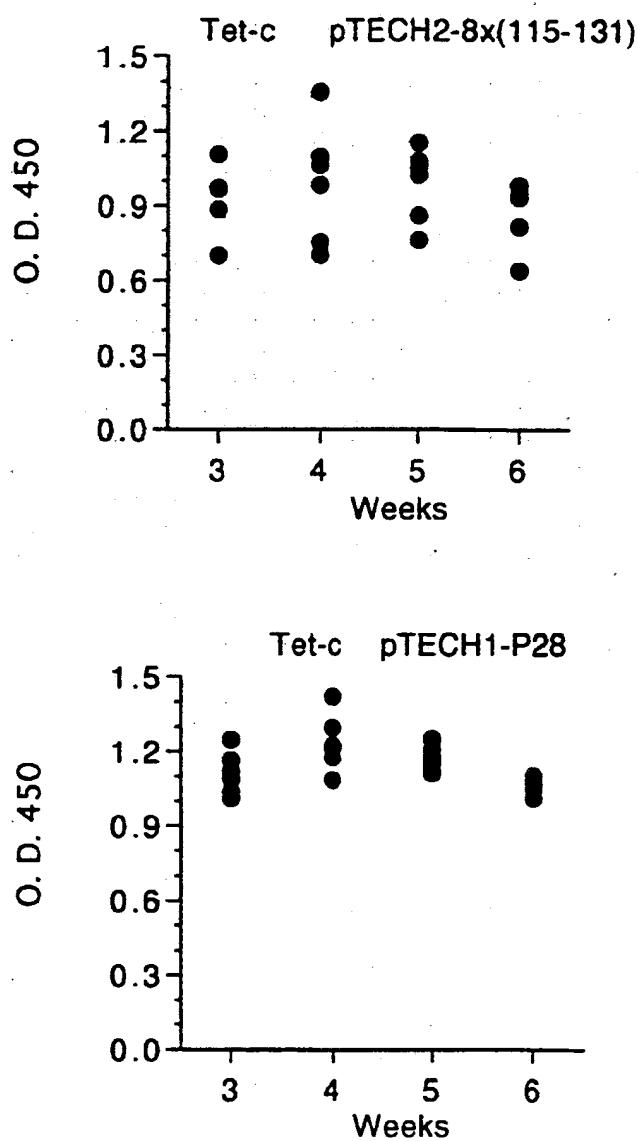


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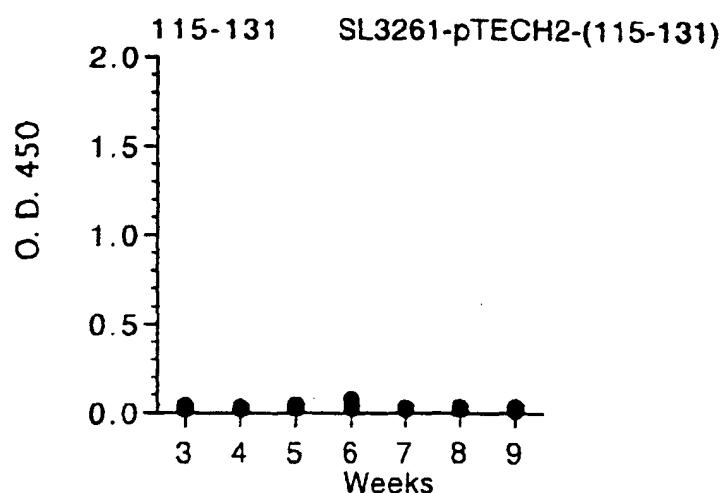
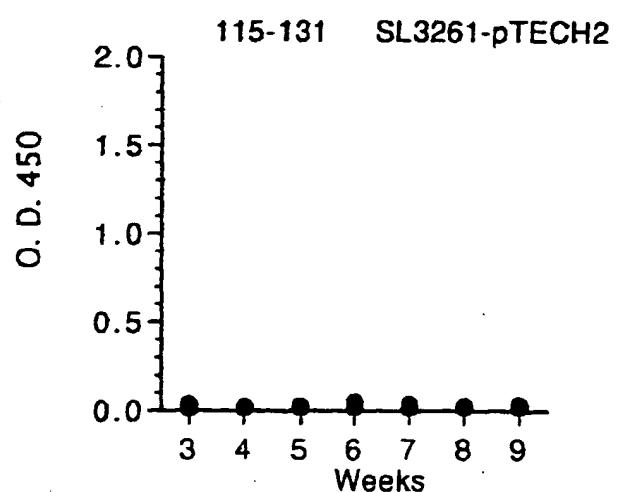
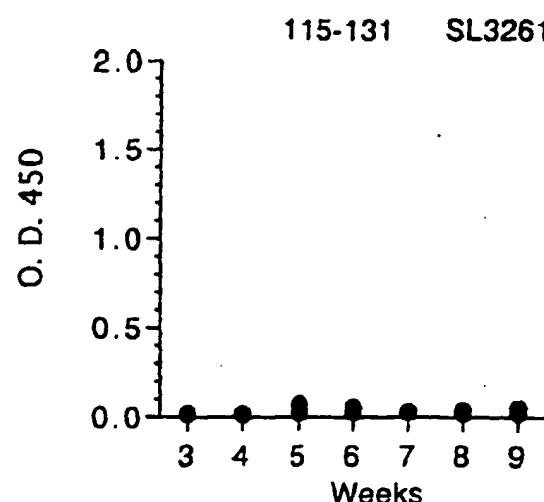


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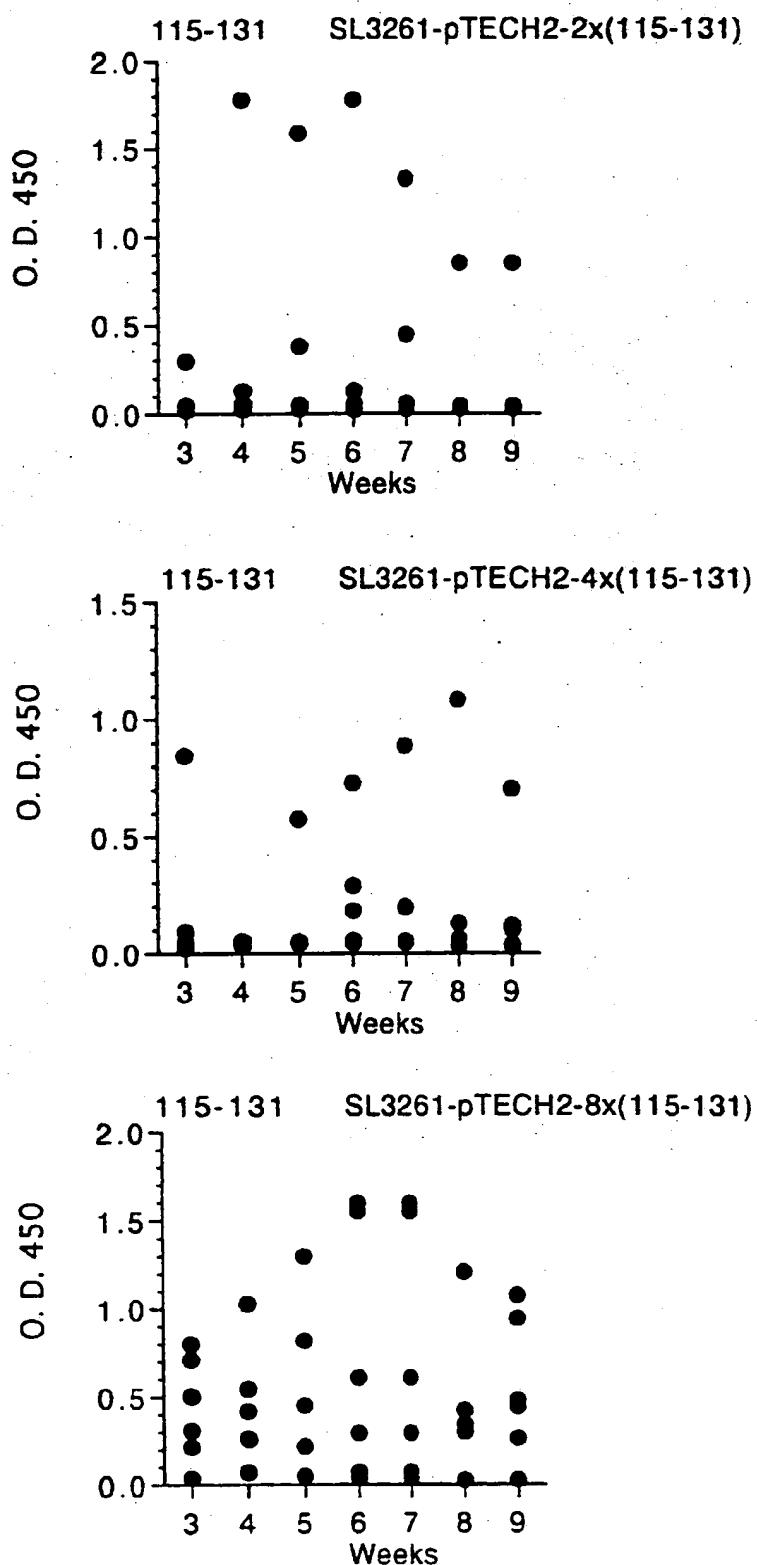


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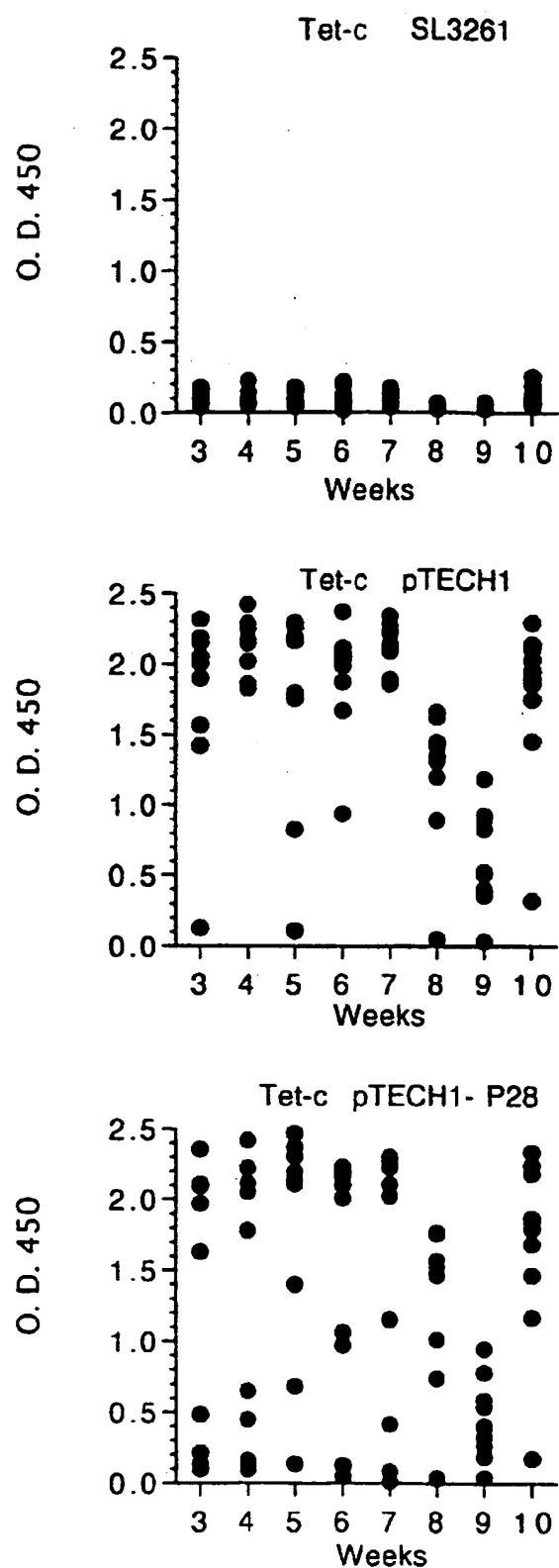
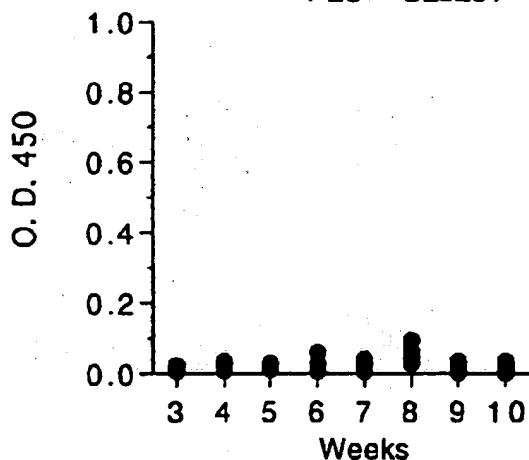
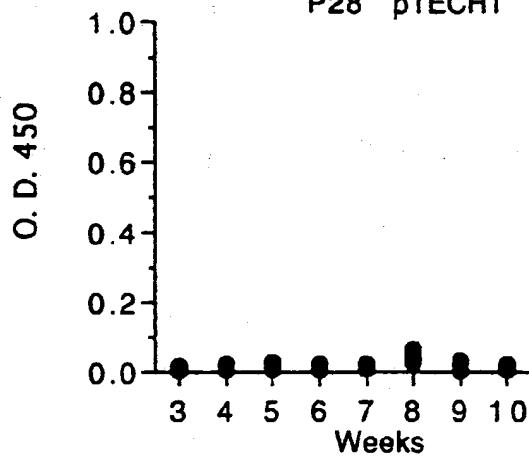


Figure 8

P28 SL3261



P28 pTECH1



P28 pTECH1-P28

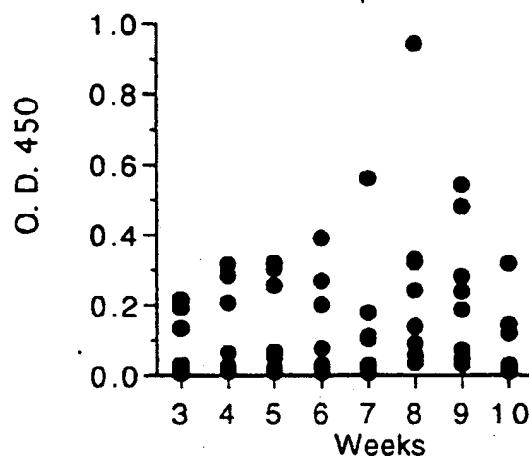


Figure 9

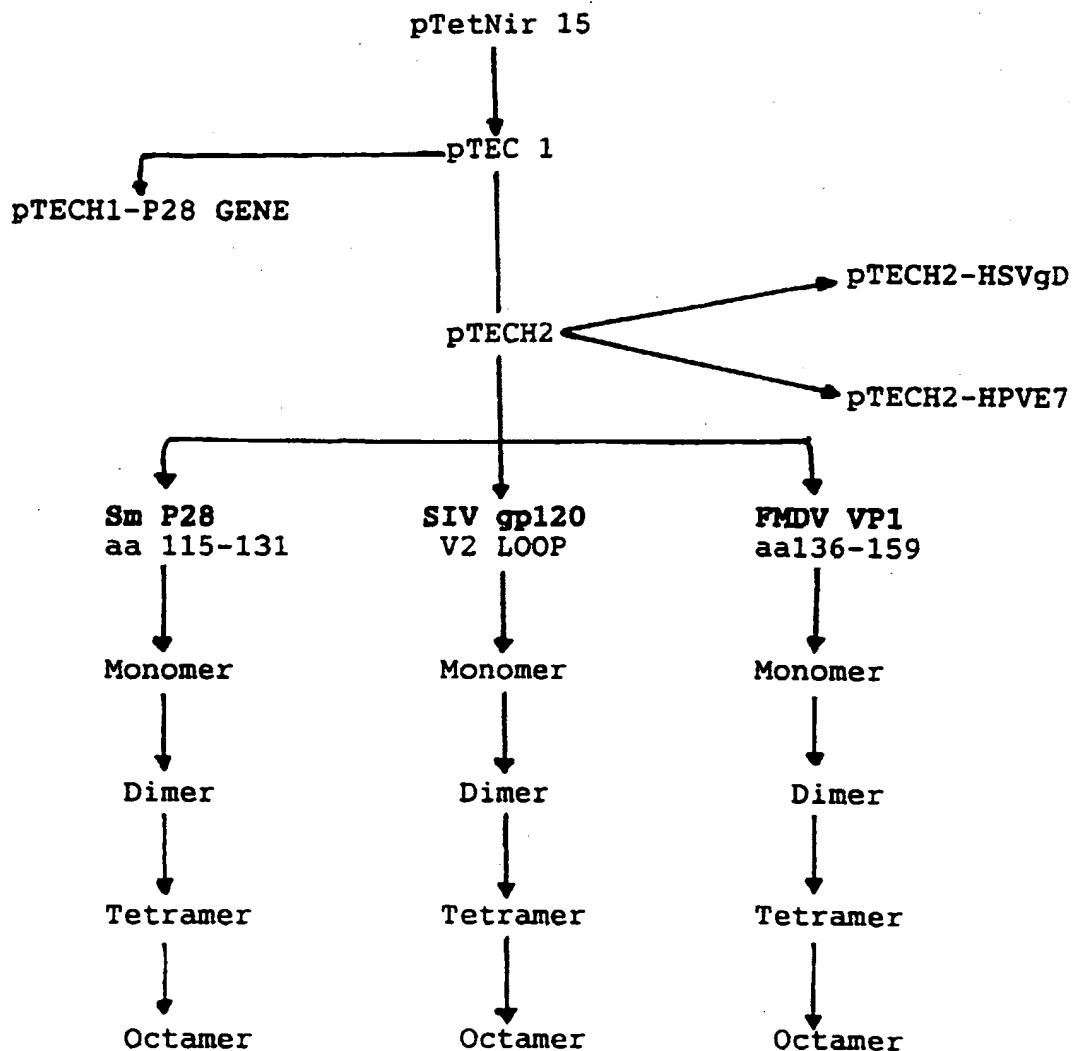
THE CONSTRUCTS

FIGURE 10

Examples of Heteromers



= *S. mansoni* P28 epitope



= SIV gp 120 V2 epitope

~ = Hinge

FIGURE 11

FIGURE 12

DNA Sequence of the Vector pTECH1

(SEQ ID NO: 17)

1bp -TTCAGGTAAATTGATGTACATCAAATGGTACCCCTTGCTGANTCGTTAAGGTAGGGGGT - 60bp

AGGGCCCAGATCTTAATCATCCACAGGAGACTTCTGATGAAAAACCTTGATTTGTTGGGT
 CGACAACGAAGAAGRCATCGATGTTATCTGAAAAGTCTACCACTCTGAACTTGGACAT
 CAACAAAGATAATTATCTCGACATCTCTGGTTCACTCCTCTGTTATCACATATCCAGA
 TGCTCAATTGGTGCCCCGGCATCAACGGCAAAGCTATCCACCTGGTTAACAAACGAATCTC
 TGAAGTTATCGTGACAAGGCCATGGACATCGAAATACAACGACATGTTCAACAACCTCAC
 CGTTAGCTCTGGCTGCGGGTCCGAAAGTTCTGCTTCCCACCTGGAACAGTACGGCAC
 TAACGAGTACTCCNTCATCAGCTCTATGAAGAAAACACTCCCTGTCCATCGGCTCTGGTTG
 GTCCTGTTCCCTGAAAGGGTAACAACCTGATCTGGACTCTGAAAGACTCCGGGGCGAAGT
 TOGTCAGATCACTTTCCGCGACCTGGCCGGCAAGTTCAACGCGTACCTGGCTAACAAATG
 GGTTTTICATCACTATCACTAACGATCGTCGCTCTGCTAACCTGTACATCAACGGGT
 TCTGATGGCTCCGCTGAAATCACTGGCTGGGGCTATCCGTGAGGACAACAACATCAC
 TCCTAAAGCTGGACCGTTGCAACAAACACACCACTACGTATCCATCGACAAGTTCCGTAT
 CTTCTGCAAAGCACTGAACCCGAAGAGATCGAAAAACTGIAATACCAGCTACCTGTCTAT
 CACCTTCCTGCGTGACTCTGGGTAAACCGCTGGGTACGACACCGAATATTACCTGAT
 CCGGTAGCTTAGCTCTAAAGACGTTCTGAAAACATCACTGACTACATGTACCT
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 CCCGAAAGACGGTAAACGTTCAACAAACCTGGACAGAAATTCTGCGTGTGGTTACACGC
 TCCGGGTATCCCGCTGTACAAAAAAATGGAAAGCTGTTAAACTGCGTGACCTGAAAACCTA
 CTCTGTTCTGAAACTGTACGACGACAAAAACGCTTCTCTGGGTCTGGTTGGTACCCA
 CAACGGTCAGATCGGTAAACGACCCGAACCGTGACATCTGATCGCTCTAACCTGGTACCT
 CAACCAACCTGAAAGACAAAATCTGGGTGGGACTGGTACCTCGTACCGACCGATGAAGG
 TTGGACCAACGACGGCCGGGGCCCTCTAGAATCACTAGTTAAGGATCGCTAGCCCGCC

pTECH1 DNA Sequence continued

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 GCAACAAACATGAATGGCTTCTGGTTTCCGTTCTGTAAGTCTGAAACGGAAACGGGAAGTCA
 GCGCTCTTCCGCTTCTCGCTACTGACTCGCTGCCCTGGTGGTCTGGCTGCCGAGC
 GGTATCAGCTCACTCAAAGGGTAATACGGTATCCACAGAAATCAGGGATAACGCAGG
 AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCT
 GGCGTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCA
 GAGGTGGCGAAACCGACAGGACTATAAGATAACCAGGCTTCCCTGGTAAGCTCCCT
 CGTGGCTCTCTGTTCCGACCCCTGCCGCTTACCGATA CCTGTCGGCTTCTCCCTTC
 GCGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCT
 TCGCTCCAAGCTGGCTGTGTCACGAACCCCCCGTTCAAGCCCCACCGCTGCCCTATC
 CGGTAACCTATGCTTGTAGTCCAACCCGTAAGACACGACTTATGCCACTGGCAGCAGC
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 GTGGCCTAACTACGGCTACACTAGAAGGACAGTATTGGTATCTGCCCTGCTGAAGCC
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 CGTOGTGTAGATAACTACGATA CGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGAT
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 GGCGAGCGCAGAAGTGGTCTGCAACTTATCGGCTCCATCCAGTCTATTAAATTGTTG

pTECH1 DNA Sequence continued

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CGGATAACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGTTCCGCGCACATTCC
CCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAA
TAGGCGTATCACGAGGCCCTTGGCTTCAAGAA - 3754bp

FIGURE 13

DNA Sequence of the Vector pTECH2

(SEQ ID NO: 18)

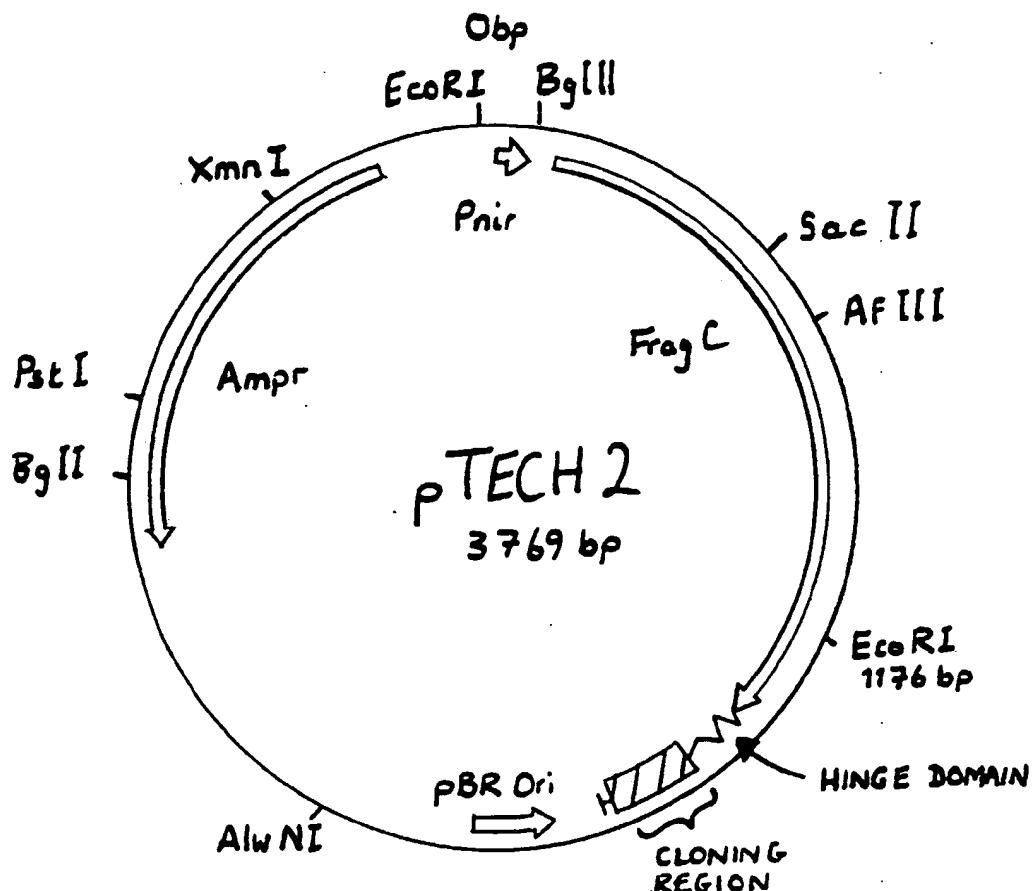
1bp - TTCAGGTAAATTGATGTACATCAATGGTACCCCTTGCTGAATCGTTAAGGTAGGGCGT - 60bp
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 CGACAACGAAGAACAGACATCGATGTTATCTGAAAAAGTCCTACCATTCTGAACCTGGACAT
 CAACAACGATATTATCTCGAACATCTCTGGTTCTAACCTCTCTGTTATCACATATCCAGA
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pTECH2 DNA Sequence continued

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 TTGCGGTAGGTCTGCTCCAAGCTGGCTGTGTCACGAACCCCCCGTTCAAGCCCGA
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XbaI BamHi EcoRV HindIII SpeI Stop BamHi

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AGATCT CCTAGG CTATAG TTCGAA TGATCA ATT ACTAG
(SEQ ID NO: 19)

---GPGP --- S R G S D I K L T S *

(SEQ ID NO: 20)

FIGURE 14